



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: P. D. CHRISTIAN, K. H. J. GORDON and
T. N. HANZLIK

(ii) TITLE OF INVENTION: INSECT VIRUSES AND THEIR USES IN
PROTECTING PLANTS

(iii) NUMBER OF SEQUENCES: 53

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: SAN FRANCISCO
(D) STATE: CALIFORNIA
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 94111

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/677,653
(B) FILING DATE: 3 OCTOBER 2000
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: RICHARD F. TRECARTIN
(B) REGISTRATION NUMBER: 31,801
(C) REFERENCE/DOCKET NUMBER: A-58631-4/RFT/NBC

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATCCACAG NNN

13

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGGCGATG CCGGCGTCGC GTTCACAG

28

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGATG CTGGAGTGGC GTCACAG

27

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAGCGAGG CCGGCGTCGC GTCACAG

27

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATCGATGC CGGACTGGTA TCCCAGGGGG

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATCGATGC CGGACTGGTA TCCCGAGGGGA C

31

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCGATGA TCCAGCCTCC TCGCGGCCGG ATGGGCA

39

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCTAGATC CATTGCCAT CGGAAGATGC CCATCCGGC

39

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCGATT ATTGCCGAGAA GGTAACCAGA GAAACACAC

39

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCTAGACC AGGTAATATA CCACAACGTG TGTTTCTCT

39

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGGGGGAATT CATTTAGGTG ACACATAGT TCTGCCTCCC CGGAC

45

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGGGGATCC TGGTATCCA GGGGGG

27

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCGGAAGCTT GTTTTCTTT CTTTACCA

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGGGGATCCG ATGGTATCCC GAGGGACGCT CAGCAGGTGG CATAGG

46

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAATAATTAA GTTACTTTAG AAGGAGATAT ACATATGAGC GAGCGAGCAC AC

52

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATAATTAA GTTTAACCTT AAGAAGGAGA TCTACATATG CTGGAGTGGC GTCAC

55

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGAGATCTAC ATATGGGAGA TGCTGGAGTG

30

(2) INFORMATION FOR SEQ ID NO:18:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAGCGAACG TCGAGAA

17

(2) INFORMATION FOR SEQ ID NO:19:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGGGGATCCT CAGTTGTCAG TGGCGGGGT A G

31

(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGGATCCCT AATTGGCACG AGCGGCAC

28

(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTACATAT GGCGGCCGCC GTTTCTGCC

29

(2) INFORMATION FOR SEQ ID NO:22:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATTACATAT GTTCGCGGCC GCCGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Phe Ala Ala Ala Val Ser Ala Phe Ala Ala Asn Met Leu Ser Ser Val
1 5 10 15
Leu Lys Ser

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Thr Leu Val Asp Gln Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu
1 5 10 15
Thr Pro Thr Ser
20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Phe Ala Ala Ala Val Ser
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCCCCUG GGAUACCAGG AUC

23

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCAGCAGGTG GCATAGG

17

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCAT ATG GGC GAT GCC GGC GTC GCG TCA CAG
Met Gly Asp Ala Gly Val Ala Ser Gln
1 5

32

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Gly Asp Ala Gly Val Ala Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCCAT ATG AGC GAG GCC GGC GTC GCG TCA CAG
Met Ser Glu Ala Gly Val Ala Ser Gln
1 5

32

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein - N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Ser Glu Ala Gly Val Ala Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..27
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG GGA GAT GCT GGA GTG GCG TCA CAG
Met Gly Asp Ala Gly Val Ala Ser Gln
1 5

27

(2) INFORMATION FOR SEQ ID NO:33:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Gly Asp Ala Gly Val Ala Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:34:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGGGATCCC GC GGATTAT GAGCGAG

27

(2) INFORMATION FOR SEQ ID NO:35:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGGATCCC GC GGAGACAT GAGCGAGCAC AC

32

(2) INFORMATION FOR SEQ ID NO:36:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGGGGATCCA GCGACATGAG AGATGCTGGA GTGG

34

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGGGATCCA GCGACATGAG AGATGCTGGA GTGG

34

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GGGGGATCCG TTCTGCCTCC CCGGAC

26

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 37..5145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTTCCTGCCTC	CCCCGGACGG	TAAATATAGG	GGAACA	ATG	TAC	GCG	AAA	GCG	ACA	Met	Tyr	Ala	Lys	Ala	Thr	54
										1					5	
GAC	GTG	GCG	CGT	GTC	TAC	GCC	GCG	GCA	GAT	GTC	GCC	TAC	GCG	AAC	GTA	102
Asp	Val	Ala	Arg	Val	Tyr	Ala	Ala	Ala	Asp	Val	Ala	Tyr	Ala	Asn	Val	
										10	15		20			
CTG	CAG	CAG	AGA	GCA	GTC	AAG	TTG	GAC	TTC	GCC	CCG	CCA	CTG	AAG	GCA	150
Leu	Gln	Gln	Arg	Ala	Val	Lys	Leu	Asp	Phe	Ala	Pro	Pro	Leu	Lys	Ala	
										25	30		35			
CTA	GAA	ACC	CTC	CAC	AGA	CTG	TAC	TAT	CCG	CTG	CGC	TTC	AAA	GGG	GGC	198
Leu	Glu	Thr	Leu	His	Arg	Leu	Tyr	Tyr	Pro	Leu	Arg	Phe	Lys	Gly	Gly	
										40	45		50			
ACT	TTA	CCC	CCG	ACA	CAA	CAC	CCG	ATC	CTG	GCC	GGG	CAC	CAA	CGT	GTC	246
Thr	Leu	Pro	Pro	Thr	Gln	His	Pro	Ile	Leu	Ala	Gly	His	Gln	Arg	Val	
										55	60		65		70	
GCA	GAA	GAG	GTT	CTG	CAC	AAT	TTC	GCC	AGG	GGA	CGT	AGC	ACA	GTG	CTC	294
Ala	Glu	Glu	Val	Leu	His	Asn	Phe	Ala	Arg	Gly	Arg	Ser	Thr	Val	Leu	
										75	80		85			

GAG ATA GGG CCG TCT CTG CAC AGC GCA CTT AAG CTA CAT GGG GCA CCG	342
Glu Ile Gly Pro Ser Leu His Ser Ala Leu Lys Leu His Gly Ala Pro	
90 95 100	
AAC GCC CCC GTC GCA GAC TAT CAC GGG TGC ACC AAG TAC GGC ACC CGC	390
Asn Ala Pro Val Ala Asp Tyr His Gly Cys Thr Lys Tyr Gly Thr Arg	
105 110 115	
GAC GGC TCG CGA CAC ATT ACG GCC TTA GAG TCT AGA TCC GTC GCC ACA	438
Asp Gly Ser Arg His Ile Thr Ala Leu Glu Ser Arg Ser Val Ala Thr	
120 125 130	
GGC CGG CCC GAG TTC AAG GCC GAC GCC TCA CTG CTC GCC AAC GGC ATT	486
Gly Arg Pro Glu Phe Lys Ala Asp Ala Ser Leu Leu Ala Asn Gly Ile	
135 140 145 150	
GCC TCC CGC ACC TTC TGC GAC GGA GTC GGC TCT TGC GCG TTC AAA	534
Ala Ser Arg Thr Phe Cys Val Asp Gly Val Gly Ser Cys Ala Phe Lys	
155 160 165	
TCG CGC GTT GGA ATT GCC AAT CAC TCC CTC TAT GAC GTG ACC CTA GAG	582
Ser Arg Val Gly Ile Ala Asn His Ser Leu Tyr Asp Val Thr Leu Glu	
170 175 180	
GAG CTG GCC AAT GCG TTT GAG AAC CAC GGA CTT CAC ATG GTC CGC GCG	630
Glu Leu Ala Asn Ala Phe Glu Asn His Gly Leu His Met Val Arg Ala	
185 190 195	
TTC ATG CAC ATG CCA GAA GAG CTG CTC TAC ATG GAC AAC GTG GTT AAT	678
Phe Met His Met Pro Glu Glu Leu Leu Tyr Met Asp Asn Val Val Asn	
200 205 210	
GCC GAG CTC GGC TAC CGC TTC CAC GTT ATT GAA GAG CCT ATG GCT GTG	726
Ala Glu Leu Gly Tyr Arg Phe His Val Ile Glu Glu Pro Met Ala Val	
215 220 225 230	
AAG GAC TGC GCA TTC CAG GGG GGG GAC CTC CGT CTC CAC TTC CCT GAG	774
Lys Asp Cys Ala Phe Gln Gly Gly Asp Leu Arg Leu His Phe Pro Glu	
235 240 245	
TTG GAC TTC ATC AAC GAG AGC CAA GAG CGG CGC ATC GAG AGG CTG GCC	822
Leu Asp Phe Ile Asn Glu Ser Gln Glu Arg Arg Ile Glu Arg Leu Ala	
250 255 260	
GCC CGC GGC TCC TAC TCC AGA CGC GCC GTC ATT TTC TCC GGC GAC GAC	870
Ala Arg Gly Ser Tyr Ser Arg Arg Ala Val Ile Phe Ser Gly Asp Asp	
265 270 275	
GAC TGG GGT GAT GCG TAC TTA CAC GAC TTC CAC ACA TGG CTC GCC TAC	918
Asp Trp Gly Asp Ala Tyr Leu His Asp Phe His Thr Trp Leu Ala Tyr	
280 285 290	
CTA CTG GTG AGG AAC TAC CCC ACT CCG TTT GGT TTC TCA CTC CAT ATA	966
Leu Leu Val Arg Asn Tyr Pro Thr Pro Phe Gly Phe Ser Leu His Ile	
295 300 305 310	
GAA GTC CAG AGG CGC CAC GGC TCC AGC ATT GAG CTG CGC ATC ACT CGC	1014
Glu Val Gln Arg Arg His Gly Ser Ser Ile Glu Leu Arg Ile Thr Arg	
315 320 325	
GCG CCA CCT GGA GAC CGC ATG CTG GCC GTC GTC CCA AGG ACG TCC CAA	1062
Ala Pro Pro Gly Asp Arg Met Leu Ala Val Val Pro Arg Thr Ser Gln	
330 335 340	
GGC CTC TGC AGA ATC CCA AAC ATC TTT TAT TAC GCC GAC GCG TCG GGC	1110
Gly Leu Cys Arg Ile Pro Asn Ile Phe Tyr Tyr Ala Asp Ala Ser Gly	
345 350 355	
ACT GAG CAT AAG ACC ATC CTT ACG TCA CAG CAC AAA GTC AAC ATG CTG	1158
Thr Glu His Lys Thr Ile Leu Thr Ser Gln His Lys Val Asn Met Leu	
360 365 370	
CTC AAT TTT ATG CAA ACG CGT CCT GAG AAG GAA CTA GTC GAC ATG ACC	1206
Leu Asn Phe Met Gln Thr Arg Pro Glu Lys Glu Leu Val Asp Met Thr	
375 380 385 390	

GTC TTG ATG TCG TTC GCG CGC GCT AGG CTG CGC GCG ATC GTG GTC GCC		1254
Val Leu Met Ser Phe Ala Arg Ala Arg Leu Arg Ala Ile Val Val Ala		
395 400 405		
TCA GAA GTC ACC GAG AGC TCC TGG AAC ATC TCA CCG GCT GAC CTG GTC		1302
Ser Glu Val Thr Glu Ser Ser Trp Asn Ile Ser Pro Ala Asp Leu Val		
410 415 420		
CGC ACT GTC GTG TCT CTT TAC GTC CTC CAC ATC ATC GAG CGC CGA AGG		1350
Arg Thr Val Val Ser Leu Tyr Val Leu His Ile Ile Glu Arg Arg Arg		
425 430 435		
GCT GCG GTC GCT GTC AAG ACC GCC AAG GAC GAC GTC TTT GGA GAG ACT		1398
Ala Ala Val Ala Val Lys Thr Ala Lys Asp Asp Val Phe Gly Glu Thr		
440 445 450		
TCG TTC TGG GAG AGT CTC AAG CAC GTC TTG GGC TCC TGT TGC GGT CTG		1446
Ser Phe Trp Glu Ser Leu Lys His Val Leu Gly Ser Cys Cys Gly Leu		
455 460 465 470		
CGC AAC CTC AAA GGC ACC GAC GTC GTC TTT ACT AAG CGC GTC GTC GAT		1494
Arg Asn Leu Lys Gly Thr Asp Val Val Phe Thr Lys Arg Val Val Asp		
475 480 485		
AAG TAC CGA GTC CAC TCG CTC GGA GAC ATA ATC TGC GAC GTC CGC CTG		1542
Lys Tyr Arg Val His Ser Leu Gly Asp Ile Ile Cys Asp Val Arg Leu		
490 495 500		
TCC CCT GAA CAG GTC GGC TTC CTG CCG TCC CGC GTA CCA CCT GCC CGC		1590
Ser Pro Glu Gln Val Gly Phe Leu Pro Ser Arg Val Pro Pro Ala Arg		
505 510 515		
GTC TTT CAC GAC AGG GAA GAG CTT GAG GTC CTT CGC GAA GCT GGC TGC		1638
Val Phe His Asp Arg Glu Glu Leu Glu Val Leu Arg Glu Ala Gly Cys		
520 525 530		
TAC AAC GAA CGT CCG GTA CCT TCC ACT CCT CCT GTG GAG GAG CCC CAA		1686
Tyr Asn Glu Arg Pro Val Pro Ser Thr Pro Pro Val Glu Glu Pro Gln		
535 540 545 550		
GGT TTC GAC GCC GAC TTG TGG CAC GCG ACC GCG GCC TCA CTC CCC GAG		1734
Gly Phe Asp Ala Asp Leu Trp His Ala Thr Ala Ala Ser Leu Pro Glu		
555 560 565		
TAC CGC GCC ACC TTG CAG GCA GGT CTC AAC ACC GAC GTC AAG CAG CTC		1782
Tyr Arg Ala Thr Leu Gln Ala Gly Leu Asn Thr Asp Val Lys Gln Leu		
570 575 580		
AAG ATC ACC CTC GAG AAC GCC CTC AAG ACC ATC GAC GGG CTC ACC CTC		1830
Lys Ile Thr Leu Glu Asn Ala Leu Lys Thr Ile Asp Gly Leu Thr Leu		
585 590 595		
TCC CCA GTC AGA GGC CTC GAG ATG TAC GAG GGC CCG CCA GGC AGC GGC		1878
Ser Pro Val Arg Gly Leu Glu Met Tyr Glu Gly Pro Pro Gly Ser Gly		
600 605 610		
AAG ACG GGC ACC CTC ATC GCC GCC CTT GAG GCC GCG GGC GGT AAA GCA		1926
Lys Thr Gly Thr Leu Ile Ala Ala Leu Glu Ala Ala Gly Gly Lys Ala		
615 620 625 630		
CTT TAC GTG GCA CCC ACC AGA GAA CTG AGA GAG GCT ATG GAC CGG CGG		1974
Leu Tyr Val Ala Pro Thr Arg Glu Leu Arg Glu Ala Met Asp Arg Arg		
635 640 645		
ATC AAA CCG CCG TCC GCC TCG GCT ACG CAA CAT GTC GCC CTT GCG ATT		2022
Ile Lys Pro Pro Ser Ala Ser Ala Thr Gln His Val Ala Leu Ala Ile		
650 655 660		
CTC CGT CGT GCC ACC GCC GAG GGC GCC CCT TTC GCT ACC GTG GTT ATC		2070
Leu Arg Arg Ala Thr Ala Glu Gly Ala Pro Phe Ala Thr Val Val Ile		
665 670 675		
GAC GAG TGC TTC ATG TTC CCG CTC GTG TAC GTC GCG ATC GTG CAC GCC		2118
Asp Glu Cys Phe Met Phe Pro Leu Val Tyr Val Ala Ile Val His Ala		
680 685 690		

TTG TCC CCG AGC TCA CGA ATA GTC CTT GTA GGG GAC GTC CAC CAA ATC Leu Ser Pro Ser Ser Arg Ile Val Leu Val Gly Asp Val His Gln Ile 695 700 705 710	2166
GGG TTT ATA GAC TTC CAA GGC ACA AGC GCG AAC ATG CCG CTC GTT CGC Gly Phe Ile Asp Phe Gln Gly Thr Ser Ala Asn Met Pro Leu Val Arg 715 720 725	2214
GAC GTC GTT AAG CAG TGC CGT CGG CGC ACT TTC AAC CAA ACC AAG CGC Asp Val Val Lys Gln Cys Arg Arg Arg Thr Phe Asn Gln Thr Lys Arg 730 735 740	2262
TGT CCG GCC GAC GTC GTT GCC ACC ACG TTT TTC CAG AGC TTG TAC CCC Cys Pro Ala Asp Val Val Ala Thr Thr Phe Phe Gln Ser Leu Tyr Pro 745 750 755	2310
GGG TGC ACA ACC ACC TCA GGG TGC GTC GCA TCC ATC AGC CAC GTC GCC Gly Cys Thr Thr Ser Gly Cys Val Ala Ser Ile Ser His Val Ala 760 765 770	2358
CCA GAC TAC CGC AAC AGC CAG GCG CAA ACG CTC TGC TTC ACG CAG GAG Pro Asp Tyr Arg Asn Ser Gln Ala Gln Thr Leu Cys Phe Thr Gln Glu 775 780 785 790	2406
GAA AAG TCG CGC CAC GGG GCT GAG GGC GCG ATG ACT GTG CAC GAA GCG Glu Lys Ser Arg His Gly Ala Glu Gly Ala Met Thr Val His Glu Ala 795 800 805	2454
CAG GGA CGC ACT TTT GCG TCT GTC ATT CTG CAT TAC AAC GGC TCC ACA Gln Gly Arg Thr Phe Ala Ser Val Ile Leu His Tyr Asn Gly Ser Thr 810 815 820	2502
GCA GAG CAG AAG CTC CTC GCT GAG AAG TCG CAC CTT CTA GTC GGC ATC Ala Glu Gln Lys Leu Ala Glu Lys Ser His Leu Leu Val Gly Ile 825 830 835	2550
ACG CGC CAC ACC AAC CAC CTG TAC ATC CGC GAC CCG ACA GGT GAC ATT Thr Arg His Thr Asn His Leu Tyr Ile Arg Asp Pro Thr Gly Asp Ile 840 845 850	2598
GAG AGA CAA CTC AAC CAT AGC GCG AAA GCC GAG GTG TTT ACA GAC ATC Glu Arg Gln Leu Asn His Ser Ala Lys Ala Glu Val Phe Thr Asp Ile 855 860 865 870	2646
CCT GCA CCC CTG GAG ATC ACG ACT GTC AAA CCG AGT GAA GAG GTG CAG Pro Ala Pro Leu Glu Ile Thr Val Lys Pro Ser Glu Glu Val Gln 875 880 885	2694
CGC AAC GAA GTG ATG GCA ACG ATA CCC CCG CAG AGT GCC ACG CCG CAC Arg Asn Glu Val Met Ala Thr Ile Pro Pro Gln Ser Ala Thr Pro His 890 895 900	2742
GGA GCA ATC CAT CTG CTC CGC AAG AAC TTC GGG GAC CAA CCC GAC TGT Gly Ala Ile His Leu Leu Arg Lys Asn Phe Gly Asp Gln Pro Asp Cys 905 910 915	2790
GGC TGT GTC GCT TTG GCG AAG ACC GGC TAC GAG GTG TTT GGC GGT CGT Gly Cys Val Ala Leu Ala Lys Thr Gly Tyr Glu Val Phe Gly Gly Arg 920 925 930	2838
GCC AAA ATC AAC GTA GAG CTT GCC GAA CCC GAC GCG ACC CCG AAG CCG Ala Lys Ile Asn Val Glu Leu Ala Glu Pro Asp Ala Thr Pro Lys Pro 935 940 945 950	2886
CAT AGG GCG TTC CAG GAA GGG GTA CAG TGG GTC AAG GTC ACC AAC GCG His Arg Ala Phe Gln Glu Gly Val Gln Trp Val Lys Val Thr Asn Ala 955 960 965	2934
TCT AAC AAA CAC CAG GCG CTC CAG ACG CTG TTG TCC CGC TAC ACC AAG Ser Asn Lys His Gln Ala Leu Gln Thr Leu Leu Ser Arg Tyr Thr Lys 970 975 980	2982
CGA AGC GCT GAC CTG CCG CTA CAC GAA GCT AAG GAG GAC GTC AAA CGC Arg Ser Ala Asp Leu Pro Leu His Glu Ala Lys Glu Asp Val Lys Arg 985 990 995	3030

ATG CTA AAC TCG CTT GAC CGA CAT TGG GAC TGG ACT GTC ACT GAA GAC Met Leu Asn Ser Leu Asp Arg His Trp Asp Trp Thr Val Thr Glu Asp 1000 1005 1010	3078
GCC CGT GAC CGA GCT GTC TTC GAG ACC CAG CTC AAG TTC ACC CAA CGC Ala Arg Asp Arg Ala Val Phe Glu Thr Gln Leu Lys Phe Thr Gln Arg 1015 1020 1025 1030	3126
GGC GGC ACC GTC GAA GAC CTG CTG GAG CCA GAC GAC CCC TAC ATC CGT Gly Gly Thr Val Glu Asp Leu Leu Glu Pro Asp Asp Pro Tyr Ile Arg 1035 1040 1045	3174
GAC ATA GAC TTC CTT ATG AAG ACT CAG CAG AAA GTG TCG CCC AAG CCG Asp Ile Asp Phe Leu Met Lys Thr Gln Gln Lys Val Ser Pro Lys Pro 1050 1055 1060	3222
ATC AAT ACG GGC AAG GTC GGG CAG GGG ATC GCC GCT CAC TCA AAG TCT Ile Asn Thr Gly Lys Val Gly Gln Gly Ile Ala Ala His Ser Lys Ser 1065 1070 1075	3270
CTC AAC TTC GTC CTC GCC GCT TGG ATA CGC ATA CTC GAG GAG ATA CTC Leu Asn Phe Val Leu Ala Ala Trp Ile Arg Ile Leu Glu Glu Ile Leu 1080 1085 1090	3318
CGT ACC GGG AGC CGC ACG GTC CGG TAC AGC AAC GGT CTC CCC GAC GAA Arg Thr Gly Ser Arg Thr Val Arg Tyr Ser Asn Gly Leu Pro Asp Glu 1095 1100 1105 1110	3366
GAA GAG GCC ATG CTG CTC GAA GCG AAG ATC AAT CAA GTC CCA CAC GCC Glu Glu Ala Met Leu Leu Glu Ala Lys Ile Asn Gln Val Pro His Ala 1115 1120 1125	3414
ACG TTC GTC TCG GCG GAC TGG ACC GAG TTT GAC ACC GCC CAC AAT AAC Thr Phe Val Ser Ala Asp Trp Thr Glu Phe Asp Thr Ala His Asn Asn 1130 1135 1140	3462
ACG AGT GAG CTG CTC TTC GCC CTT TTA GAG CGC ATC GGC ACG CCT Thr Ser Glu Leu Leu Phe Ala Ala Leu Leu Glu Arg Ile Gly Thr Pro 1145 1150 1155	3510
GCA GCT GCC GTT AAT CTA TTC AGA GAA CGG TGT GGG AAA CGC ACC TTG Ala Ala Ala Val Asn Leu Phe Arg Glu Arg Cys Gly Lys Arg Thr Leu 1160 1165 1170	3558
CGA GCG AAG GGT CTA GGC TCC GTT GAA GTC GAC GGT CTG CTC GAC TCC Arg Ala Lys Gly Leu Gly Ser Val Glu Val Asp Gly Leu Leu Asp Ser 1175 1180 1185 1190	3606
GGC GCA GCT TGG ACG CCT TGC CGC AAC ACC ATC TTC TCT GCC GCC GTC Gly Ala Ala Trp Thr Pro Cys Arg Asn Thr Ile Phe Ser Ala Ala Val 1195 1200 1205	3654
ATG CTC ACG CTC TTC CGC GGC GTC AAG TTC GCA GCT TTC AAA GGC GAC Met Leu Thr Leu Phe Arg Gly Val Lys Phe Ala Ala Phe Lys Gly Asp 1210 1215 1220	3702
GAC TCG CTC CTC TGT GGT AGC CAT TAC CTC CGT TTC GAC GCT AGC CGC Asp Ser Leu Leu Cys Gly Ser His Tyr Leu Arg Phe Asp Ala Ser Arg 1225 1230 1235	3750
CTT CAC ATG GGC GAA CGT TAC AAG ACC AAA CAT TTG AAG GTC GAG GTG Leu His Met Gly Glu Arg Tyr Lys Thr Lys His Leu Lys Val Glu Val 1240 1245 1250	3798
CAG AAA ATC GTG CCG TAC ATC GGA CTC CTC GTC TCC GCT GAG CAG GTC Gln Lys Ile Val Pro Tyr Ile Gly Leu Leu Val Ser Ala Glu Gln Val 1255 1260 1265 1270	3846
GTC CTC GAC CCT GTC AGG AGC GCT CTC AAG ATA TTT GGG CGC TGC TAC Val Leu Asp Pro Val Arg Ser Ala Leu Lys Ile Phe Gly Arg Cys Tyr 1275 1280 1285	3894
ACA AGC GAA CTC CTT TAC TCC AAG TAC GTG GAG GCT GTG AGA GAC ATC Thr Ser Glu Leu Leu Tyr Ser Lys Tyr Val Glu Ala Val Arg Asp Ile 1290 1295 1300	3942

ACC AAG GGC TGG AGT GAC GCC CGC TAC CAC AGC CTC CTG TGC CAC ATG		3990
Thr Lys Gly Trp Ser Asp Ala Arg Tyr His Ser Leu Leu Cys His Met		
1305 1310 1315		
TCA GCA TGC TAC TAC AAT TAC GCG CCG GAG TCT GCG GCG TAC ATC ATC		4038
Ser Ala Cys Tyr Tyr Asn Tyr Ala Pro Glu Ser Ala Ala Tyr Ile Ile		
1320 1325 1330		
GAC GCT GTT GTT CGC TTT GGG CGC GGC GAC TTC CCG TTT GAA CAA CTG		4086
Asp Ala Val Val Arg Phe Gly Arg Gly Asp Phe Pro Phe Glu Gln Leu		
1335 1340 1345 1350		
CGC GTG GTG CGT GCC CAT GTG CAG GCA CCC GAC GCT TAC AGC AGC ACG		4134
Arg Val Val Arg Ala His Val Gln Ala Pro Asp Ala Tyr Ser Ser Thr		
1355 1360 1365		
TAT CCG GCT AAC GTG CGC GCA TCG TGC CTT GAC CAC GTC TTC GAG CCC		4182
Tyr Pro Ala Asn Val Arg Ala Ser Cys Leu Asp His Val Phe Glu Pro		
1370 1375 1380		
CGC CAG GCC GCC CCG GCA GGT TTC GTT GCG ACA TGT GCG AAG CCG		4230
Arg Gln Ala Ala Ala Pro Ala Gly Phe Val Ala Thr Cys Ala Lys Pro		
1385 1390 1395		
GAA ACG CCT TCT TCA CTT ACC GCG AAA GCT GGT GTT TCT GCG ACT ACA		4278
Glu Thr Pro Ser Ser Leu Thr Ala Lys Ala Gly Val Ser Ala Thr Thr		
1400 1405 1410		
AGC CAC GTT GCG ACT GGG ACT GCG CCC CCG GAG TCT CCA TGG GAT GCA		4326
Ser His Val Ala Thr Gly Thr Ala Pro Pro Glu Ser Pro Trp Asp Ala		
1415 1420 1425 1430		
CCT GCA GCC AAC AGC TTT TCG GAG TTA TTG ACA CCG GAG ACC CCG TCC		4374
Pro Ala Ala Asn Ser Phe Ser Glu Leu Leu Thr Pro Glu Thr Pro Ser		
1435 1440 1445		
ACA TCA TCC TCG CCG TCA TCG TCT TCA TCG GAC TCC TCT ACA TCG TGT		4422
Thr Ser Ser Pro Ser Ser Ser Ser Asp Ser Ser Thr Ser Cys		
1450 1455 1460		
GGA AGG TCG CTC AGT GGT GGA GAC ACC GCA AGG ACC ACA GAA GAC TTG		4470
Gly Arg Ser Leu Ser Gly Gly Asp Thr Ala Arg Thr Thr Glu Asp Leu		
1465 1470 1475		
AAC AGC AGA AAG CCG CCT TCG CAA GAC AGG CAA TCA CGC TCG TCT GAA		4518
Asn Ser Arg Lys Pro Pro Ser Gln Asp Arg Gln Ser Arg Ser Ser Glu		
1480 1485 1490		
TGT CTG GAC AGA AGC GGA GAA AGG ACA GGC AGT TCG TTA ACT GCC CCC		4566
Cys Leu Asp Arg Ser Gly Glu Arg Thr Gly Ser Ser Leu Thr Ala Pro		
1495 1500 1505 1510		
ACT GCT CCG AGC CCC TCA TTC TCA TTT TCG GAA AGA GCT CGA CTG GCG		4614
Thr Ala Pro Ser Pro Ser Phe Ser Phe Ser Glu Arg Ala Arg Leu Ala		
1515 1520 1525		
ACC GGG CCG ACT GTC GCC GCT GCG ACA TCA CCT TCG GCA ACC CCA TCC		4662
Thr Gly Pro Thr Val Ala Ala Ala Thr Ser Pro Ser Ala Thr Pro Ser		
1530 1535 1540		
TGC GCC ACG GAC CAG GTT GCC GCG AGG ACC ACG CCG GAC TTT GCG CCT		4710
Cys Ala Thr Asp Gln Val Ala Ala Arg Thr Thr Pro Asp Phe Ala Pro		
1545 1550 1555		
TTC CTG GGT TCC CAG TCT GCC CGT GCT GTC TCG AAG CCG TAC CGG CCC		4758
Phe Leu Gly Ser Gln Ser Ala Arg Ala Val Ser Lys Pro Tyr Arg Pro		
1560 1565 1570		
CCC ACG ACT GCC CGT TGG AAA GAA GTC ACC CCG CTC CAC GCG TGG AAG		4806
Pro Thr Thr Ala Arg Trp Lys Glu Val Thr Pro Leu His Ala Trp Lys		
1575 1580 1585 1590		
GGC GTG ACC GGA GAC CGA CCG GAA GTC AGG GAG GAC CCG GAG ACA GCG		4854
Gly Val Thr Gly Asp Arg Pro Glu Val Arg Glu Asp Pro Glu Thr Ala		
1595 1600 1605		

GCG GTC GTC CAG GCT CTG ATC AGC GGC CGT TAT CCT CAG AAG ACG AAG Ala Val Val Gln Ala Leu Ile Ser Gly Arg Tyr Pro Gln Lys Thr Lys 1610 1615 1620	4902
CTT TCC TCC GAC GCA TCC AAA GGC TAC TCA AGA ACT AAG GGA TGC TCA Leu Ser Ser Asp Ala Ser Lys Gly Tyr Ser Arg Thr Lys Gly Cys Ser 1625 1630 1635	4950
CAA TCC ACC TCT TTT CCT GCC CCG AGT GCG GAT TAC CAG GCC CGC GAC Gln Ser Thr Ser Phe Pro Ala Pro Ser Ala Asp Tyr Gln Ala Arg Asp 1640 1645 1650	4998
TGC CAG ACA GTC CGA GTC TGC CGC GCC GCT GCA GAG ATG GCG CGC TCA Cys Gln Thr Val Arg Val Cys Arg Ala Ala Glu Met Ala Arg Ser 1655 1660 1665 1670	5046
TGT ATT CAC GAG CCG TTG GCT TCA TCT GCC GCC AGT GAC TTG AAG Cys Ile His Glu Pro Leu Ala Ser Ser Ala Ala Ser Ala Asp Leu Lys 1675 1680 1685	5094
CGC ATA CGC TCT ACC TCG GAC TCT GTT CCC GAT GTA AAG ATC AGC AAG Arg Ile Arg Ser Thr Ser Asp Ser Val Pro Asp Val Lys Ile Ser Lys 1690 1695 1700	5142
AGC GCA TGAAGGAACA AAATTAGTTT CCTTGTTCGT AAACAAGGTG GTCCCTCCCCA Ser Ala	5198
TTGAGGTAAA GACTCTGGTG AGTCCTCAAC GTTACTCGTT GAGTCTGCTG CGGTTCGATT CCATTCCCAA GCAGCAAAGG GTGCGCAACT AGTACGGCGC CCCCTGGGAT ACCA	5258 5312

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1704 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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Met Tyr Ala Lys Ala Thr Asp Val Ala Arg Val Tyr Ala Ala Asp
1 5 10 15
Val Ala Tyr Ala Asn Val Leu Gln Gln Arg Ala Val Lys Leu Asp Phe
20 25 30
Ala Pro Pro Leu Lys Ala Leu Glu Thr Leu His Arg Leu Tyr Tyr Pro
35 40 45
Leu Arg Phe Lys Gly Gly Thr Leu Pro Pro Thr Gln His Pro Ile Leu
50 55 60
Ala Gly His Gln Arg Val Ala Glu Glu Val Leu His Asn Phe Ala Arg
65 70 75 80
Gly Arg Ser Thr Val Leu Glu Ile Gly Pro Ser Leu His Ser Ala Leu
85 90 95
Lys Leu His Gly Ala Pro Asn Ala Pro Val Ala Asp Tyr His Gly Cys
100 105 110
Thr Lys Tyr Gly Thr Arg Asp Gly Ser Arg His Ile Thr Ala Leu Glu
115 120 125
Ser Arg Ser Val Ala Thr Gly Arg Pro Glu Phe Lys Ala Asp Ala Ser
130 135 140
Leu Leu Ala Asn Gly Ile Ala Ser Arg Thr Phe Cys Val Asp Gly Val
145 150 155 160
Gly Ser Cys Ala Phe Lys Ser Arg Val Gly Ile Ala Asn His Ser Leu
165 170 175
Tyr Asp Val Thr Leu Glu Glu Leu Ala Asn Ala Phe Glu Asn His Gly
180 185 190
Leu His Met Val Arg Ala Phe Met His Met Pro Glu Glu Leu Leu Tyr

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195	200	205
Met Asp Asn Val Val Asn Ala Glu Leu Gly Tyr Arg Phe His Val Ile		
210	215	220
Glu Glu Pro Met Ala Val Lys Asp Cys Ala Phe Gln Gly Gly Asp Leu		
225	230	235
Arg Leu His Phe Pro Glu Leu Asp Phe Ile Asn Glu Ser Gln Glu Arg		
245	250	255
Arg Ile Glu Arg Leu Ala Ala Arg Gly Ser Tyr Ser Arg Arg Ala Val		
260	265	270
Ile Phe Ser Gly Asp Asp Trp Gly Asp Ala Tyr Leu His Asp Phe		
275	280	285
His Thr Trp Leu Ala Tyr Leu Leu Val Arg Asn Tyr Pro Thr Pro Phe		
290	295	300
Gly Phe Ser Leu His Ile Glu Val Gln Arg Arg His Gly Ser Ser Ile		
305	310	315
Glu Leu Arg Ile Thr Arg Ala Pro Pro Gly Asp Arg Met Leu Ala Val		
325	330	335
Val Pro Arg Thr Ser Gln Gly Leu Cys Arg Ile Pro Asn Ile Phe Tyr		
340	345	350
Tyr Ala Asp Ala Ser Gly Thr Glu His Lys Thr Ile Leu Thr Ser Gln		
355	360	365
His Lys Val Asn Met Leu Leu Asn Phe Met Gln Thr Arg Pro Glu Lys		
370	375	380
Glu Leu Val Asp Met Thr Val Leu Met Ser Phe Ala Arg Ala Arg Leu		
385	390	395
Arg Ala Ile Val Val Ala Ser Glu Val Thr Glu Ser Ser Trp Asn Ile		
405	410	415
Ser Pro Ala Asp Leu Val Arg Thr Val Val Ser Leu Tyr Val Leu His		
420	425	430
Ile Ile Glu Arg Arg Ala Ala Val Ala Val Lys Thr Ala Lys Asp		
435	440	445
Asp Val Phe Gly Glu Thr Ser Phe Trp Glu Ser Leu Lys His Val Leu		
450	455	460
Gly Ser Cys Cys Gly Leu Arg Asn Leu Lys Gly Thr Asp Val Val Phe		
465	470	475
Thr Lys Arg Val Val Asp Lys Tyr Arg Val His Ser Leu Gly Asp Ile		
485	490	495
Ile Cys Asp Val Arg Leu Ser Pro Glu Gln Val Gly Phe Leu Pro Ser		
500	505	510
Arg Val Pro Pro Ala Arg Val Phe His Asp Arg Glu Glu Leu Glu Val		
515	520	525
Leu Arg Glu Ala Gly Cys Tyr Asn Glu Arg Pro Val Pro Ser Thr Pro		
530	535	540
Pro Val Glu Glu Pro Gln Gly Phe Asp Ala Asp Leu Trp His Ala Thr		
545	550	555
Ala Ala Ser Leu Pro Glu Tyr Arg Ala Thr Leu Gln Ala Gly Leu Asn		
565	570	575
Thr Asp Val Lys Gln Leu Lys Ile Thr Leu Glu Asn Ala Leu Lys Thr		
580	585	590
Ile Asp Gly Leu Thr Leu Ser Pro Val Arg Gly Leu Glu Met Tyr Glu		
595	600	605
Gly Pro Pro Gly Ser Gly Lys Thr Gly Thr Leu Ile Ala Ala Leu Glu		
610	615	620
Ala Ala Gly Gly Lys Ala Leu Tyr Val Ala Pro Thr Arg Glu Leu Arg		
625	630	635
Glu Ala Met Asp Arg Arg Ile Lys Pro Pro Ser Ala Ser Ala Thr Gln		
645	650	655

His Val Ala Leu Ala Ile Leu Arg Arg Ala Thr Ala Glu Gly Ala Pro
 660 665 670
 Phe Ala Thr Val Val Ile Asp Glu Cys Phe Met Phe Pro Leu Val Tyr
 675 680 685
 Val Ala Ile Val His Ala Leu Ser Pro Ser Ser Arg Ile Val Leu Val
 690 695 700
 Gly Asp Val His Gln Ile Gly Phe Ile Asp Phe Gln Gly Thr Ser Ala
 705 710 715 720
 Asn Met Pro Leu Val Arg Asp Val Val Lys Gln Cys Arg Arg Arg Thr
 725 730 735
 Phe Asn Gln Thr Lys Arg Cys Pro Ala Asp Val Val Ala Thr Thr Phe
 740 745 750
 Phe Gln Ser Leu Tyr Pro Gly Cys Thr Thr Thr Ser Gly Cys Val Ala
 755 760 765
 Ser Ile Ser His Val Ala Pro Asp Tyr Arg Asn Ser Gln Ala Gln Thr
 770 775 780
 Leu Cys Phe Thr Gln Glu Glu Lys Ser Arg His Gly Ala Glu Gly Ala
 785 790 795 800
 Met Thr Val His Glu Ala Gln Gly Arg Thr Phe Ala Ser Val Ile Leu
 805 810 815
 His Tyr Asn Gly Ser Thr Ala Glu Gln Lys Leu Leu Ala Glu Lys Ser
 820 825 830
 His Leu Leu Val Gly Ile Thr Arg His Thr Asn His Leu Tyr Ile Arg
 835 840 845
 Asp Pro Thr Gly Asp Ile Glu Arg Gln Leu Asn His Ser Ala Lys Ala
 850 855 860
 Glu Val Phe Thr Asp Ile Pro Ala Pro Leu Glu Ile Thr Thr Val Lys
 865 870 875 880
 Pro Ser Glu Glu Val Gln Arg Asn Glu Val Met Ala Thr Ile Pro Pro
 885 890 895
 Gln Ser Ala Thr Pro His Gly Ala Ile His Leu Leu Arg Lys Asn Phe
 900 905 910
 Gly Asp Gln Pro Asp Cys Gly Cys Val Ala Leu Ala Lys Thr Gly Tyr
 915 920 925
 Glu Val Phe Gly Gly Arg Ala Lys Ile Asn Val Glu Leu Ala Glu Pro
 930 935 940
 Asp Ala Thr Pro Lys Pro His Arg Ala Phe Gln Glu Gly Val Gln Trp
 945 950 955 960
 Val Lys Val Thr Asn Ala Ser Asn Lys His Gln Ala Leu Gln Thr Leu
 965 970 975
 Leu Ser Arg Tyr Thr Lys Arg Ser Ala Asp Leu Pro Leu His Glu Ala
 980 985 990
 Lys Glu Asp Val Lys Arg Met Leu Asn Ser Leu Asp Arg His Trp Asp
 995 1000 1005
 Trp Thr Val Thr Glu Asp Ala Arg Asp Arg Ala Val Phe Glu Thr Gln
 1010 1015 1020
 Leu Lys Phe Thr Gln Arg Gly Gly Thr Val Glu Asp Leu Leu Glu Pro
 1025 1030 1035 1040
 Asp Asp Pro Tyr Ile Arg Asp Ile Asp Phe Leu Met Lys Thr Gln Gln
 1045 1050 1055
 Lys Val Ser Pro Lys Pro Ile Asn Thr Gly Lys Val Gly Gln Gly Ile
 1060 1065 1070
 Ala Ala His Ser Lys Ser Leu Asn Phe Val Leu Ala Ala Trp Ile Arg
 1075 1080 1085
 Ile Leu Glu Glu Ile Leu Arg Thr Gly Ser Arg Thr Val Arg Tyr Ser
 1090 1095 1100
 Asn Gly Leu Pro Asp Glu Glu Ala Met Leu Leu Glu Ala Lys Ile

1105	1110	1115	1120
Asn Gln Val Pro His Ala Thr Phe Val Ser Ala Asp Trp Thr Glu Phe			
1125	1130	1135	
Asp Thr Ala His Asn Asn Thr Ser Glu Leu Leu Phe Ala Ala Leu Leu			
1140	1145	1150	
Glu Arg Ile Gly Thr Pro Ala Ala Val Asn Leu Phe Arg Glu Arg			
1155	1160	1165	
Cys Gly Lys Arg Thr Leu Arg Ala Lys Gly Leu Gly Ser Val Glu Val			
1170	1175	1180	
Asp Gly Leu Leu Asp Ser Gly Ala Ala Trp Thr Pro Cys Arg Asn Thr			
1185	1190	1195	1200
Ile Phe Ser Ala Ala Val Met Leu Thr Leu Phe Arg Gly Val Lys Phe			
1205	1210	1215	
Ala Ala Phe Lys Gly Asp Asp Ser Leu Leu Cys Gly Ser His Tyr Leu			
1220	1225	1230	
Arg Phe Asp Ala Ser Arg Leu His Met Gly Glu Arg Tyr Lys Thr Lys			
1235	1240	1245	
His Leu Lys Val Glu Val Gln Lys Ile Val Pro Tyr Ile Gly Leu Leu			
1250	1255	1260	
Val Ser Ala Glu Gln Val Val Leu Asp Pro Val Arg Ser Ala Leu Lys			
1265	1270	1275	1280
Ile Phe Gly Arg Cys Tyr Thr Ser Glu Leu Leu Tyr Ser Lys Tyr Val			
1285	1290	1295	
Glu Ala Val Arg Asp Ile Thr Lys Gly Trp Ser Asp Ala Arg Tyr His			
1300	1305	1310	
Ser Leu Leu Cys His Met Ser Ala Cys Tyr Tyr Asn Tyr Ala Pro Glu			
1315	1320	1325	
Ser Ala Ala Tyr Ile Ile Asp Ala Val Val Arg Phe Gly Arg Gly Asp			
1330	1335	1340	
Phe Pro Phe Glu Gln Leu Arg Val Val Arg Ala His Val Gln Ala Pro			
1345	1350	1355	1360
Asp Ala Tyr Ser Ser Thr Tyr Pro Ala Asn Val Arg Ala Ser Cys Leu			
1365	1370	1375	
Asp His Val Phe Glu Pro Arg Gln Ala Ala Ala Pro Ala Gly Phe Val			
1380	1385	1390	
Ala Thr Cys Ala Lys Pro Glu Thr Pro Ser Ser Leu Thr Ala Lys Ala			
1395	1400	1405	
Gly Val Ser Ala Thr Thr Ser His Val Ala Thr Gly Thr Ala Pro Pro			
1410	1415	1420	
Glu Ser Pro Trp Asp Ala Pro Ala Ala Asn Ser Phe Ser Glu Leu Leu			
1425	1430	1435	1440
Thr Pro Glu Thr Pro Ser Thr Ser Ser Pro Ser Ser Ser Ser Ser			
1445	1450	1455	
Asp Ser Ser Thr Ser Cys Gly Arg Ser Leu Ser Gly Gly Asp Thr Ala			
1460	1465	1470	
Arg Thr Thr Glu Asp Leu Asn Ser Arg Lys Pro Pro Ser Gln Asp Arg			
1475	1480	1485	
Gln Ser Arg Ser Ser Glu Cys Leu Asp Arg Ser Gly Glu Arg Thr Gly			
1490	1495	1500	
Ser Ser Leu Thr Ala Pro Thr Ala Pro Ser Pro Ser Phe Ser Phe Ser			
1505	1510	1515	1520
Glu Arg Ala Arg Leu Ala Thr Gly Pro Thr Val Ala Ala Ala Thr Ser			
1525	1530	1535	
Pro Ser Ala Thr Pro Ser Cys Ala Thr Asp Gln Val Ala Ala Arg Thr			
1540	1545	1550	
Thr Pro Asp Phe Ala Pro Phe Leu Gly Ser Gln Ser Ala Arg Ala Val			
1555	1560	1565	

Ser Lys Pro Tyr Arg Pro Pro Thr Thr Ala Arg Trp Lys Glu Val Thr
 1570 1575 1580
 Pro Leu His Ala Trp Lys Gly Val Thr Gly Asp Arg Pro Glu Val Arg
 1585 1590 1595 1600
 Glu Asp Pro Glu Thr Ala Ala Val Val Gln Ala Leu Ile Ser Gly Arg
 1605 1610 1615
 Tyr Pro Gln Lys Thr Lys Leu Ser Ser Asp Ala Ser Lys Gly Tyr Ser
 1620 1625 1630
 Arg Thr Lys Gly Cys Ser Gln Ser Thr Ser Phe Pro Ala Pro Ser Ala
 1635 1640 1645
 Asp Tyr Gln Ala Arg Asp Cys Gln Thr Val Arg Val Cys Arg Ala Ala
 1650 1655 1660
 Ala Glu Met Ala Arg Ser Cys Ile His Glu Pro Leu Ala Ser Ser Ala
 1665 1670 1675 1680

 Ala Ser Ala Asp Leu Lys Arg Ile Arg Ser Thr Ser Asp Ser Val Pro
 1685 1690 1695
 Asp Val Lys Ile Ser Lys Ser Ala
 1700

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4218..4512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTTCTGCCCTC	CCCCGGACGG	TAAATATAGG	GGAACAAATGT	ACCGCAAAGC	GACAGACGTG	60
GCGCGTGTCT	ACGCCCGGGC	AGATGTCGCC	TACCGAACG	TACTGCAGCA	GAGAGCAGTC	120
AAGTTGGACT	TCGCCCCGCC	ACTGAAGGCA	CTAGAAACCC	TCCACAGACT	GTACTATCCG	180
CTGCGCTTCA	AAGGGGGCAC	TTTACCCCCG	ACACAACACC	CGATCCTGGC	CGGGCACCAA	240
CGTGTCCGAG	AAGAGGTTCT	GCACAATTTC	GCCAGGGGAC	GTAGCACAGT	GCTCGAGATA	300
GGGCCGTCTC	TGCACAGCGC	ACTTAAGCTA	CATGGGGCAC	CGAACGCC	CGTCGAGAC	360
TATCACGGGT	GCACCAAGTA	CGGCACCCCGC	GACGGCTCGC	GACACATTAC	GGCCTTAGAG	420
TCTAGATCCG	TCGCCACAGG	CCGGCCCGAG	TTCAAGCCG	ACGCCTCACT	GCTCGCCAAC	480
GGCATTGCCCT	CCCGCACCTT	CTGCGTCGAC	GGAGTCGGCT	CTTGCCTCGTT	CAAATCGCGC	540
GTTGGAATTG	CCAATCACTC	CCTCTATGAC	GTGACCCCTAG	AGGAGCTGGC	CAATGCGTTT	600
GAGAACACG	GACTTCACAT	GGTCCGCGCG	TTCATGCACA	TGCCAGAAGA	GCTGCTCTAC	660
ATGGACAAACG	TGGTTAATGC	CGAGCTCGGC	TACCGCTTCC	ACGTTATTGA	AGAGCCTATG	720
GCTGTGAAGG	ACTGCCATT	CCAGGGGGGG	GACCTCCGTC	TCCACTTCCC	TGAGTTGGAC	780
TTCATCAACG	AGAGCCAAGA	GCGGCGCATC	GAGAGGCTGG	CCGCCCGGG	CTCCTACTCC	840
AGACGCGCCG	TCATTTCTC	CGCGACGAC	GACTGGGTG	ATGCGTACTT	ACACGACTTC	900
CACACATGGC	TCGCCTACCT	ACTGGTGAGG	AACTACCCA	CTCCGTTTGG	TTTCTCACTC	960
CATATAGAACG	TCCAGAGGCG	CCACGGCTCC	AGCATTGAGC	TGCGCATCAC	TCGCGCGCCA	1020
CCTGGAGACC	GCATGCTGGC	CGTCGTCCCA	AGGACGTCCC	AAGGCCTCTG	CAGAATCCCA	1080
AAACATCTTT	ATTACGCCGA	CGCGTCGGGC	ACTGAGCATA	AGACCATCCT	TACGTCACAG	1140
CACAAAAGTC	ACATGCTGCT	CAATTTATG	CAAACGGC	CTGAGAAGGA	ACTAGTCGAC	1200
ATGACCGTCT	TGATGTCGTT	CGCGCGCGCT	AGGCTGCGC	CGATCGTGGT	CGCCTCAGAA	1260
GTCACCGAGA	GCTCCTGGAA	CATCTCACCG	GCTGACCTGG	TCCGCACTGT	CGTGTCTCTT	1320
TACGTCCCTCC	ACATCATCGA	GCGCCGAAGG	GCTGCGGTG	CTGTCAAGAC	CGCCAAGGAC	1380
GACGTCTTTG	GAGAGACTTC	GTTCTGGGAG	AGTCTCAAGC	ACGTCTTGGG	CTCCTGTTGC	1440
GGTCTGCGCA	ACCTCAAAGG	CACCGACGTC	GTCTTACTA	AGCGCGTCG	CGATAAGTAC	1500

GTC TTC ATC GGA CTC CTC TAC ATC GTG TGG AAG GTC GCT CAG TGG TGG	4442
Val Phe Ile Gly Leu Leu Tyr Ile Val Trp Lys Val Ala Gln Trp Trp	
60 65 70 75	
AGA CAC CGC AAG GAC CAC AGA AGA CTT GAA CAG CAG AAA GCC GCC TTC	4490
Arg His Arg Lys Asp His Arg Arg Leu Glu Gln Gln Lys Ala Ala Phe	
80 85 90	
GCA AGA CAG GCA ATC ACG CTC GTC TGAATGTC TGGACAGAAG CGGAGAAAGG	4542
Ala Arg Gln Ala Ile Thr Leu Val	
95	
ACAGGCAGTT CGTTAACTGC CCCCACGTGCT CCGAGCCCT CATTCTCATT TTGGAAAGA	4602
GCTCGACTGG CGACCGGGCC GACTGTCGCC GCTGCGACAT CACCTTCGGC AACCCCATCC	4662
TGCGCCACGG ACCAGGTTGC CGCGAGGACC ACGCCGGACT TTGCGCCTT CCTGGGTTCC	4722
CAGTCTGCC GTGCTGTCTC GAAGCCGTAC CGGCCCTCCA CGACTGCCCG TTGGAAAGAA	4782
GTCACCCCGC TCCACCGCGT GAAGGGCGTG ACCGGAGACC GACCGGAAGT CAGGGAGGAC	4842
CCGGAGACAG CGGCAGTCGT CCAGGCTCTG ATCAGCGGCC GTTATCCTCA GAAGACGAAG	4902
CTTCCCTCCG ACGCATCAA AGGCTACTCA AGAACTAAGG GATGCTCACA ATCCACCTCT	4962
TTTCCTGCC CGAGTGCAGA TTACCAAGGCC CGCGACTGCC AGACAGTCCG AGTCTGCCGC	5022
GCCGCTGCAG AGATGGCGCG CTCATGTATT CACGAGCCGT TGCGTTCATC TGCGCCAGT	5082
GCCGACTTGA AGCGCATACG CTCTACCTCG GACTCTGTT CCGATGTAAA GATCAGCAAG	5142
AGCGCATGAA GGAACAAAAT TAGTTCCCTT GTTCGTAAAC AAGGTGGTCC CTCCCATGTA	5202
GGTAAAGACT CTGGTGAGTC CTCAACGTTA CTCGTTGAGT CTGCTGCCGT TCGATTCCAT	5262
TCCCAAGCAG CAAAGGGTGC GCAACTAGTA CGGCCCTCCCC TGGAATACCA	5312

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Met Cys Glu Ala Gly Asn Ala Phe Phe Thr Tyr Arg Glu Ser Trp Cys
 1           5          10          15
Phe Cys Asp Tyr Lys Pro Arg Cys Asp Trp Asp Cys Ala Pro Gly Val
 20          25          30
Ser Met Gly Cys Thr Cys Ser Gln Gln Leu Phe Gly Val Ile Asp Thr
 35          40          45
Gly Asp Pro Val His Ile Ile Leu Ala Val Ile Val Phe Ile Gly Leu
 50          55          60
Leu Tyr Ile Val Trp Lys Val Ala Gln Trp Trp Arg His Arg Lys Asp
 65          70          75          80
His Arg Arg Leu Glu Gln Gln Lys Ala Ala Phe Ala Arg Gln Ala Ile
 85          90          95
Thr Leu Val

```

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4518..4937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTTCTGCCTC	CCCCGGACGG	TAAATATAGG	GGAACAATGT	ACGCAGAAAGC	GACAGACGTG	60
GCGCGTGTCT	ACGCCCGGGC	AGATGTCGCC	TACGCGAACG	TACTGCAGCA	GAGAGCAGTC	120
AAGTTGGACT	TCGCCCCGCC	ACTGAAGGCA	CTAGAAACCC	TCCACAGACT	GTACTATCCG	180
CTGCGCTTCA	AAGGGGGCAC	TTTACCCCCG	ACACAACACC	CGATCCTGGC	CGGGCACCAA	240
CGTGTGCGAG	AAGAGGTTCT	GCACAATTTC	GCCAGGGGAC	GTAGCACAGT	GCTCGAGATA	300
GGGCCGTCTC	TGCACAGCGC	ACTTAAGCTA	CATGGGGCAC	CGAACGCC	CGTCGAGAC	360
TATCACGGGT	GCACCAAGTA	CGGCACCCGC	GACGGCTCGC	GACACATTAC	GGCCTTAGAG	420
TCTAGATCCG	TCGCCACAGG	CCGGCCCCGAG	TTCAAGGCCG	ACGCCTCACT	GCTCGCAAC	480
GGCATTGCCCT	CCCGCACCTT	CTGCGTCGAC	GGAGTCGGCT	TTGCGCGTT	CAAATCGCGC	540
GTGGAATTG	CCAATCACTC	CCTCTATGAC	GTGACCCCTAG	AGGAGCTGGC	CAATCGCTT	600
GAGAACCAACG	GACTTCACAT	GGTCCGCGCG	TTCATGCACA	TGCCAGAAGA	GCTGCTCTAC	660
ATGGACAACG	TGGTTAATGC	CGAGCTCGGC	TACCGCTTCC	ACGTTATTGA	AGAGCCTATG	720
GCTGTGAAGG	ACTGCGCATT	CCAGGGGGGG	GACCTCCGTC	TCCACTTCCC	TGAGTTGGAC	780
TTCATCAACG	AGAGCCAAGA	GCGGCGCATC	GAGAGGCTGG	CCGCCCGGG	CTCCTACTCC	840
AGACGCGCCG	TCATTTCCTC	CGGCGACGAC	GAETGGGTG	ATGCGTACTT	ACACGACTTC	900
CACACATGGC	TCGCCTACCT	ACTGGTGAGG	AACTACCCCA	CTCCGTTGG	TTTCTCACTC	960
CATATAGAAG	TCCAGAGGCG	CCACGGCTCC	AGCATTGAGC	TGCGCATCAC	TCGCGCGCCA	1020
CCTGGAGACC	GCATGCTGGC	CGTCGCTCCA	AGGACGTCCC	AAGGCCTCTG	CAGAATCCCA	1080
AACATCTTT	ATTACGCCGA	CGCGTCGGGC	ACTGAGCATA	AGACCATCCT	TACGTCACAG	1140
CACAAAGTCA	ACATGCTGCT	CAATTTATG	CAAACGCGTC	CTGAGAAGGA	ACTAGTCGAC	1200
ATGACCGTCT	TGATGTCGTT	CGCGCCGCGT	AGGCTGCGCG	CGATCGTGGT	CGCCTCAGAA	1260
GTCACCGAGA	GCTCCTGGAA	CATCTCACCG	GCTGACCTGG	TCCGCACTGT	CGTGTCTCTT	1320
TACGTCCCTCC	ACATCATCGA	GCGCCGAAGG	GCTGCGGTG	CTGTCAGAC	CGCCAAGGAC	1380
GACGTCTTG	GAGAGACTTC	GTTCTGGGAG	AGTCTCAAGC	ACGTCTTGGG	CTCCTGTTGC	1440
GGTCTGCGCA	ACCTCAAAGG	CACCGACGTC	GTCTTACTA	AGCGCGTCGT	CGATAAGTAC	1500
CGAGTCCACT	CGCTCGGAGA	CATAATCTGC	GACGTCCGCC	TGTCCCCTGA	ACAGGTCGGC	1560
TTCCTGCCGT	CCCGCGTACC	ACCTGCCCGC	GTCTTCACG	ACAGGGAAGA	GCTTGAGGTC	1620
CTTCGCGAAG	CTGGCTGCTA	CAACGAACGT	CCGGTACCTT	CCACTCCTCC	TGTGGAGGAG	1680
CCCCAAGGTT	TCGACGCCGA	CTTGTGGCAC	GCGACCGCGG	CCTCACTCCC	CGAGTACCGC	1740
GCCACCTTGC	AGGCAGGTCT	CAACACCGAC	GTCAAGCAGC	TCAAGATCAC	CCTCGAGAAC	1800
GCCCTCAAGA	CCATCGACGG	GCTCACCCCTC	TCCCCAGTCA	GAGGCCTCGA	GATGTACGAG	1860
GGCCCGCCAG	GCAGCGGCAA	GACGGGCACC	CTCATCGCCG	CCCTTGAGGC	CGCGGGCGGT	1920
AAAGCACTTT	ACGTGGCACC	CACCAAGAGAA	CTGAGAGAGG	CTATGGACCG	CGGGATCAAA	1980
CCGCCGTCCG	CCTCGGCTAC	GCAACATGTC	GCCCTTGCAG	TTCTCCGTG	TGCCACCGCC	2040
GAGGGCGCCC	CTTCGCTAC	CGTGGTTATC	GACGAGTGCT	TCATGTTCCC	GCTCGTGTAC	2100
GTCGCGATCG	TGCACGCCCTT	GTCCCCGAGC	TCACGAATAG	TCCTTGTAGG	GGACGTCCAC	2160
CAAATCGGGT	TTATAGACTT	CCAAGGCACA	AGCGCGAAC	TGCCGCTCGT	TCGCGACGTC	2220
GTAAAGCAGT	GCCGTCGGCG	CACTTCAAC	CAAACCAAGC	GCTGTCCGGC	CGACGTCGTT	2280
GCCACCACGT	TTTCCAGAG	CTTGTACCCC	GGGTGCACAA	CCACCTCAGG	GTGCGTCGCA	2340
TCCATCAGCC	ACGTGCCCCC	AGACTACCAC	AACAGCCAGG	CGCAAACGCT	CTGCTTCACG	2400
CAGGAGGAAA	AGTCGCGCCA	CGGGCTGAG	GGCGCGATGA	CTGTGCACGA	AGCGCAGGG	2460
CGCACTTTG	CGTCTGTCT	TCTGCATTAC	AACGGCTCCA	CAGCAGAGCA	GAAGCTCCTC	2520
GCTGAGAAGT	CGCACCTTCT	AGTCGGCATE	ACGCGCCACA	CCAACCACCT	GTACATCCGC	2580
GACCCGACAG	GTGACATTGA	GAGACAACTC	AACCATAGCG	CGAAAGCCGA	GGTGTTCACA	2640
GACATCCCTG	CACCCCTGGA	GATCACGACT	GTCAAACCGA	GTGAAGAGGT	CGAGCGAAC	2700
GAAGTGTAGG	CAACGATACC	CCCGCAGAGT	GCCACGCCGC	ACGGAGCAAT	CCATCTGCTC	2760
CGCAAGAACT	TCGGGGACCA	ACCCGACTGT	GGCTGTGTCG	CTTGGCGAA	GACCGGCTAC	2820
GAGGTGTTTG	CGGGCTGTGC	CAAATCAAC	GTAGAGCTTG	CCGAACCCGA	CGCGACCCCG	2880
AAGCCGCATA	GGGCGTCCA	GGAAAGGGTA	CAGTGGGTCA	AGGTCAACAA	CGCGTCTAAC	2940
AAACACCAGG	CGCTCCAGAC	GCTGTTGTCC	CGCTACACCA	AGCGAAGCCG	TGACCTGCCG	3000
CTACACGAAG	CTAAGGAGGA	CGTCAAACCC	ATGCTAAACT	CGCTTGACCG	ACATTGGGAC	3060
TGGACTGTCA	CTGAAGACGC	CCGTGACCGA	GCTGCTTCG	AGACCCAGCT	CAAGTTCAC	3120
CAACCGGGCG	GCACCGTCGA	AGACCTGCTG	GAGCCAGACG	ACCCCTACAT	CCGTGACATA	3180
GACTTCCTTA	TGAAGACTCA	GCAGAAAGTG	TCGCCAAGC	CGATCAATAC	GGGCAAGGTC	3240
GGCCAGGGGA	TCGCCGCTCA	CTCAAAGTCT	CTCAACTTCG	TCCTCGCCGC	TTGGATAACGC	3300
ATACTCGAGG	AGATACTCCG	TACCGGGAGC	CGCACGGTCC	GGTACAGCAA	CGGTCTCCCC	3360

GACGAAGAAG	AGGCCATGCT	GCTCGAAGCG	AAGATCAATC	AAGTCCCACA	CGCCACGTT	3420
GTCTCGCGG	ACTGGACCGA	TTTGACACC	GCCCACAATA	ACACGAGTGA	GCTGCTCTTC	3480
GCCGCCCTT	TAGAGCGCAT	CGGCACGCT	GCAGCTGCCG	TTAATCTATT	CAGAGAACGG	3540
TGTGGGAAAC	GCACCTTGC	AGCGAAGGGT	CTAGGCTCCG	TTGAAGTCGA	CGGTCTGCTC	3600
GACTCCGGCG	CAGCTGGAC	GCCTTGCCG	AACACCATCT	TCTCTGCCG	CGTCATGCTC	3660
ACGCTCTTCC	GCGCGTCAA	TTTCGAGCT	TTCAAAGGCG	ACGACTCGCT	CCTCTGTGGT	3720
AGCCATTACC	TCCGTTTCA	CGCTAGCCG	CTTCACATGG	GCGAACGTTA	CAAGACCAAA	3780
CATTGAAGG	TCGAGGTGCA	AAAATCGTG	CCGTACATCG	GACTCCTCGT	CTCCGCTGAG	3840
CAGGTCGTC	TCGACCCGT	CAGGAGCGCT	CTCAAGATAT	TTGGGCGCTG	CTACACAAGC	3900
GAACCTCTT	ACTCCAAGTA	CGTGGAGGCT	GTGAGAGACA	TCACCAAGGG	CTGGAGTGAC	3960
GCCCGCTACC	ACAGCCTCT	GTGCCACATG	TCAGCATGCT	ACTACAATTA	CGGCCGGAG	4020
TCTCGGGCGT	ACATCATCGA	CGCTGTTGTT	CGCTTGGG	GCGCGACTT	CCCGTTGAA	4080
CAACTGCGCG	TGGTGCCTGC	CCATGTGCA	GCACCCGACG	CTTACAGCAG	CACGTATCCG	4140
GCTAACGTGC	GCGCATCGT	CCTTGACCAC	GTCTCGAGC	CCC GCCAGGC	CGCCGCCCG	4200
GCAGGTTTCG	TTGCACATG	TGCGAAGCCG	GAAACGCC	CTTCACTTAC	CGCGAAAGCT	4260
GGTGTTCCTG	CGACTACAAG	CCACGTTGCG	ACTGGGACTG	CGCCCCCGGA	GTCTCCATGG	4320
GATGCACCTG	CAGCCAACAG	CTTTTCGGAG	TTATTGACAC	CGGAGACCCC	GTCCACATCA	4380
TCCTCGCCGT	CATCGTCTC	ATCGGACTCC	TCTACATCGT	GTGGAGGTC	GCTCAGTGGT	4440
GGAGACACCG	CAAGGACAC	AGAAGACTTG	AACAGCAGAA	AGCCGCCTC	GCAAGACAGG	4500
CAATCACGCT	CGTCTGA	ATG TCT GGA	CAG AAG CGG	AGA AAG GAC	AGG CAG	4550
		Met Ser Gly Gln Lys Arg Arg Lys Asp Arg Gln				
		1 5 10				
TTC GTT AAC TGC CCC CAC TGC TCC GAG CCC CTC ATT CTC ATT TTC GGA						4598
Phe Val Asn Cys Pro His Cys Ser Glu Pro Leu Ile Leu Ile Phe Gly						
15 20 25						
AAG AGC TCG ACT GGC GAC CGG GCC GAC TGT CGC CGC TGC GAC ATC ACC						4646
Lys Ser Ser Thr Gly Asp Arg Ala Asp Cys Arg Arg Cys Asp Ile Thr						
30 35 40						
TTC GGC AAC CCC ATC CTG CGC CAC GGA CCA GGT TGC CGC GAG GAC CAC						4694
Phe Gly Asn Pro Ile Leu Arg His Gly Pro Gly Cys Arg Glu Asp His						
45 50 55						
GCC GGA CTT TGC GCC TTT CCT GGG TTC CCA GTC TGC CCG TGC TGT CTC						4742
Ala Gly Leu Cys Ala Phe Pro Gly Phe Pro Val Cys Pro Cys Cys Leu						
60 65 70 75						
GAA GCC GTA CCG GCC CCC CAC GAC TGC CCG TTG GAA AGA AGT CAC CCC						4790
Glu Ala Val Pro Ala Pro His Asp Cys Pro Leu Glu Arg Ser His Pro						
80 85 90						
GCT CCA CGC GTG GAA GGG CGT GAC CGG AGA CCG ACC GGA AGT CAG GGA						4838
Ala Pro Arg Val Glu Gly Arg Asp Arg Arg Pro Thr Gly Ser Gln Gly						
95 100 105						
GGA CCC GGA GAC AGC GGC GGT CGT CCA GGC TCT GAT CAG CGG CCG TTA						4886
Gly Pro Gly Asp Ser Gly Gly Arg Pro Gly Ser Asp Gln Arg Pro Leu						
110 115 120						
TCC TCA GAA GAC GAA GCT TTC CTC CGA CGC ATC CAA AGG CTA CTC AAG						4934
Ser Ser Glu Asp Glu Ala Phe Leu Arg Arg Ile Gln Arg Leu Leu Lys						
125 130 135						
AAC TAAGGGATGC TCACAATCCA CCTCTTTCC TGCCCCGAGT GCGGATTACC						4987
Asn						
140						
AGGCCCGCGA CTGCCAGACA GTCCGAGTCT GCCGCCGCCG TGCAGAGATG GCGCGCTCAT						5047
GTATTACGA GCCGTTGGCT TCATCTGCCG CCAGTGCCG CTTGAAGCGC ATACGCTCTA						5107
CCTCGGACTC TGTCCCGAT GTAAAGATCA GCAAGAGCGC ATGAAGGAAC AAAATTAGTT						5167
TCCTTGTTCG TAAACAAAGGT GGTCCTCCC ATTGAGGTAA AGACTCTGGT GAGTCCTCAA						5227
CGTTACTCGT TGAGTCTGCT GCGGTTCGAT TCCATTCCCA AGCAGCAAAG GGTGCGCAAC						5287
TAGTACGGCG CCCCTGGGA TACCA						5312

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Met Ser Gly Gln Lys Arg Arg Lys Asp Arg Gln Phe Val Asn Cys Pro
1 5 10 15
His Cys Ser Glu Pro Leu Ile Leu Ile Phe Gly Lys Ser Ser Thr Gly
20 25 30
Asp Arg Ala Asp Cys Arg Arg Cys Asp Ile Thr Phe Gly Asn Pro Ile
35 40 45
Leu Arg His Gly Pro Gly Cys Arg Glu Asp His Ala Gly Leu Cys Ala
50 55 60
Phe Pro Gly Phe Pro Val Cys Pro Cys Cys Leu Glu Ala Val Pro Ala
65 70 75 80
Pro His Asp Cys Pro Leu Glu Arg Ser His Pro Ala Pro Arg Val Glu
85 90 95
Gly Arg Asp Arg Arg Pro Thr Gly Ser Gln Gly Gly Pro Gly Asp Ser
100 105 110
Gly Gly Arg Pro Gly Ser Asp Gln Arg Pro Leu Ser Ser Glu Asp Glu
115 120 125
Ala Phe Leu Arg Arg Ile Gln Arg Leu Leu Lys Asn
130 135 140

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4944..5162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTTCTGCCCTC	CCCCGGACGG	TAAATATAAGG	GGAACAATGT	ACCGCAAAGC	GACAGACGTG	60
GCGCGTGTCT	ACGCCGCAGC	AGATGTCGCC	TACGCAACG	TACTGCAGCA	GAGAGCAGTC	120
AAGTTGGACT	TCGCCCCGCC	ACTGAAGGCA	CTAGAAACCC	TCCACAGACT	GTACTATCCG	180
CTGCGCTTCA	AAGGGGGCAC	TTTACCCCCG	ACACAAACACC	CGATCCTGGC	CGGGCACCAA	240
CGTGTGCGAG	AAGAGGTTCT	GCACAATTTC	GCCAGGGGAC	GTAGCACAGT	GCTCGAGATA	300
GGGCCGTCTC	TGCACAGCGC	ACTTAAGCTA	CATGGGGCAC	CGAACGCC	CGTCGAGAC	360
TATCACGGGT	GCACCAAGTA	CGGCACCCCG	GACGGCTCGC	GACACATTAC	GGCCTTAGAG	420
TCTAGATCCG	TCGCCACAGG	CCGGCCCGAG	TTCAAGGCCG	ACGCCTCACT	GCTCGCCAAC	480
GGCATTGCCT	CCCGCACCTT	CTGCGTCGAC	GGAGTCGGCT	CTTGCGCGTT	CAAATCGCGC	540
GTTGGAATTG	CCAATCACTC	CCTCTATGAC	GTGACCCCTAG	AGGAGCTGGC	CAATCGTTT	600
GAGAACACCG	GACTTCACAT	GGTCCCGCG	TTCATGCACA	TGCCAGAAGA	GCTGCTCTAC	660
ATGGACAAACG	TGGTTAATGC	CGAGCTCGGC	TACCGCTTCC	ACGTTATTGA	AGAGCCTATG	720
GCTGTGAAGG	ACTGCCATT	CCAGGGGGGG	GACCTCCGTC	TCCACTTCCC	TGAGTTGGAC	780
TTCATCAACG	AGAGCCAAGA	GCGGCCATC	GAGAGGCTGG	CCGCCCCGGG	CTCCCTACTCC	840
AGACGCGCCG	TCATTTCTC	CGCGACGAC	GACTGGGGTG	ATGCGTACTT	ACACGACTTC	900
CACACATGGC	TCGCCTACCT	ACTGGTGAGG	AACTACCCCA	CTCCGTTGG	TTTCTCACTC	960
CATATAGAACG	TCCAGAGGCG	CCACGGCTCC	AGCATTGAGC	TGCGCATCAC	TCGCGCGCCA	1020
CCTGGAGACC	GCATGCTGGC	CGTCGTCCCA	AGGACGTCCC	AAGGCCTCTG	CAGAATCCCA	1080
AACATCTTTT	ATTACGCCGA	CGCGTCGGGC	ACTGAGCATA	AGACCATCCT	TACGTCACAG	1140

CACAAAGTCA	ACATGCTGCT	CAATTATG	CAAACCGTC	CTGAGAAGGA	ACTAGTCGAC	1200
ATGACCGTCT	TGATGTCGTT	CGCGCGCGT	AGGCTGCGCG	CGATCGTGGT	CGCCCTCAGAA	1260
GTCACCGAGA	GCTCTGGAA	CATCTCACCG	GCTGACCTGG	TCCGCACGTG	CGTGTCTCTT	1320
TACGTCTCC	ACATCATCGA	GCGCCGAAGG	GCTGCGGTG	CTGTCAAGAC	CGCCAAGGAC	1380
GACGTCTTG	GAGAGACTTC	GTTCTGGGAG	AGTCTCAAGC	ACGTCTTGGG	CTCCTGTTGC	1440
GGTCTGCGCA	ACCTCAAAGG	CACCGACGTC	GTCTTACTA	AGCGCGTCGT	CGATAAGTAC	1500
CGAGTCCACT	CGCTCGGAGA	CATAATCTGC	GACGTCCGCC	TGTCCCCTGA	ACAGGTCGGC	1560
TTCCCTGCCGT	CCCGCGTACC	ACCTGCCCGC	GTCTTCACG	ACAGGGAAGA	GCTTGAGGTC	1620
CTTCGCGAAG	CTGGCTGCTA	CAACGAACGT	CCGGTACCTT	CCACTCCCTC	TGTGGAGGAG	1680
CCCCAAGGTT	TCGACGCCGA	CTTGTGGCAC	GCGACCAGGG	CCTCACTCCC	CGAGTACCGC	1740
GCCACCTTGC	AGGCAGGTCT	CAACACCGAC	GTCAAGCAGC	TCAAGATCAC	CCTCGAGAAC	1800
GCCCTCAAGA	CCATCGACGG	GCTCACCCCTC	TCCCCAGTCA	GAGGCCTCGA	GATGTACGAG	1860
GGCCCGCCAG	GCAGCGGCAA	GACGGGCACC	CTCATCGCCG	CCCTTGAGGC	CGGGGGCGGT	1920
AAAGCACTT	ACGTGGCACC	CACCAAGAGAA	CTGAGAGAGG	CTATGGACCG	CGGGATCAAA	1980
CCGCCGTCCG	CCTCGGCTAC	GCAACATGTC	GCCCTTGCAG	TTCTCCGTG	TGCCACCGCC	2040
GAGGGCGCCC	CTTCGCTAC	CGTGGTTATC	GACGAGTGCT	TCATGTTCCC	GCTCGTGTAC	2100
GTCGCGATCG	TGCACGCCCT	GTCCCCGAGC	TCACGAATAG	TCCTTGTAGG	GGACGTCCAC	2160
CAAATCGGGT	TTATAGACTT	CCAAGGCACA	AGCGCGAAC	TGCGCTCGT	TGCCGACGTC	2220
GTAAAGCAGT	GCCGTCGGCG	CACTTCAAC	CAAACCAAGC	GCTGTCCGGC	CGACGTGTT	2280
GCCACCACGT	TTTTCAGAG	CTTGTACCCC	GGGTGCACAA	CCACCTCAGG	GTGCGTCGCA	2340
TCCATCAGCC	ACGTGCCCCC	AGACTACCGC	AACAGCCAGG	CGCAAACGCT	CTGCTTCACG	2400
CAGGAGGAAA	AGTCGGCCA	CGGGGCTGAG	GGCGCGATGA	CTGTGCACGA	AGCGCAGGGA	2460
CGCACTTTG	CGTCTGTCAT	TCTGCATTAC	AACGGCTCCA	CAGCAGAGCA	GAAGCTCCTC	2520
GCTGAGAAGT	CGCACCTCT	AGTCGGCATC	ACGCCACACA	CCAACCACCT	GTACATCCGC	2580
GACCCGACAG	GTGACATTGA	GAGACAACTC	AACCATAGCG	CGAAAGCCGA	GGTGTTCACA	2640
GACATCCCTG	CACCCCTGGA	GATCACGACT	GTCAAACCGA	GTGAAGAGGT	GCAGCGCAAC	2700
GAAGTGATGG	CAACGATACC	CCCGCAGAGT	GCCACGCCGC	ACGGAGCAAT	CCATCTGCTC	2760
CGCAAGAACT	TCGGGGACCA	ACCCGACTGT	GGCTGTGTCG	CTTGGCGAA	GACCGGCTAC	2820
GAGGTGTTG	CGGGTCGTG	CAAATCAAC	GTAGAGCTG	CCGAACCCGA	CGCGACCCCG	2880
AAGCCGCATA	GGGCGTTCCA	GBAAGGGGTA	CAGTGGTCA	AGGTCACCAA	CGCGCTAAC	2940
AAACACCAGG	CGCTCCAGAC	GCTGTTGTCC	CGCTACACCA	AGCGAAGCGC	TGACCTGCCG	3000
CTACACGAAG	CTAAGGAGGA	CGTCAAACGC	ATGCTAAACT	CGCTTGACCG	ACATTGGGAC	3060
TGGACTGTCA	CTGAAGACGC	CCGTGACCGA	GCTGTCTTCG	AGACCCAGCT	CAAGTTCAC	3120
CAACCGGGCG	GCACCGTCGA	AGACCTGCTG	GAGCCAGACG	ACCCCTACAT	CCGTGACATA	3180
GAECTCCTTA	TGAAGACTCA	GCAGAAAGTG	TCGCCCAAGC	CGATCAATAC	GGGAAGGTC	3240
GGCAGGGGA	TCGCCGCTCA	CTCAAAGTCT	CTCAACTTCG	TCCTCGCCGC	TTGGATAACGC	3300
ATACTCGAGG	AGATACTCCG	TACCGGGAGC	CGCACGGTCC	GGTACAGCAA	CGGTCTCCCC	3360
GACGAAGAAG	AGGCCATGCT	GCTCGAAGCG	AAGATCAATC	AAAGTCCCACA	CGCCACGTTC	3420
GTCTCGGC	ACTGGACCGA	GTTCGACACC	GCCCCACAATA	ACACGAGTGA	GCTGCTCTTC	3480
GCCGCCCTT	TAGAGCGCAT	CGGCACGCC	GCAGCTGCCG	TTAATCTATT	CAGAGAACGG	3540
TGTGGAAAC	GCACCTTGC	AGCGAAGGGT	CTAGGCTCCG	TTGAAGTCGA	CGGTCTGTC	3600
GAECTCGGCG	CAGCTTGGAC	GCCTTGC	AAACCATCT	TCTCTGCCGC	CGTCATGTC	3660
ACGCTCTCC	CGGGCGTCAA	GTTCGAGCT	TTCAAAGGCG	ACGACTCGCT	CCTCTGTGGT	3720
AGCCATTACC	TCCGTTTCGA	CGCTAGCCG	CTTCACATGG	GGGAACGTTA	CAAGACAAA	3780
CATTGAGG	TCGAGGTGCA	AAAAATCGT	CCGTACATCG	GACTCCTCGT	CTCCGCTGAG	3840
CAGGTCGTCC	TCGACCCCTG	CAGGAGCGCT	CTCAAGATAT	TTGGGCGCTG	CTACACAAGC	3900
GAACTCCTT	ACTCCAAGTA	CGTGGAGGCT	GTGAGAGACA	TCACCAAGGG	CTGGAGTGAC	3960
GCCCGCTACC	ACAGCCTCT	GTGCCACATG	TCAGCATGCT	ACTACAATT	CGGCCGGAG	4020
TCTCGGGCGT	ACATCATCGA	CGCTGTTGTT	CGCTTGGC	CGGGCGACTT	CCCGTTGAA	4080
CAACTGCGCG	TGGTGC	CCATGTGCA	GCACCCGACG	CTTACAGCAG	CACGTATCG	4140
GCTAACGTG	GCGCATCGT	CCTTGACCA	GTCTCGAGC	CCGCCAGGC	CGCCGCCCG	4200
GCAGGTTTCG	TTGGACATG	TGCGAAGCCG	GAAACGCC	CTTCACTTAC	CGCGAAAGCT	4260
GGTGTTCG	CGACTACAAG	CCACGTTGCG	ACTGGGACTG	CGCCCCCGGA	GTCTCCATGG	4320
GATGCACCTG	CAGCCAACAG	CTTTGCGGAG	TTATTGACAC	CGGAGACCCC	GTCCACATCA	4380
TCCCTGCCGT	CATCGTCTTC	ATCGGACTCC	TCTACATCGT	GTGGAAGGTC	GCTCAGTGGT	4440
GGAGACACCG	CAAGGACAC	AGAAGACTTG	AACAGCAGAA	AGCCGCCCTC	GCAAGACAGG	4500
CAATCACGCT	CGTCTGAATG	TCTGGACAGA	AGCGGAGAAA	GGACAGGCAG	TTCGTTAACT	4560

GCCCCCACTG	CTCCGAGCCC	CTCATTCTCA	TTTCGGAAA	GAGCTCGACT	GGCGACCGGG	4620
CCGACTGTG	CCGCTGCGAC	ATCACCTTCG	GCAACCCAT	CCTGCGCCAC	GGACCAGGTT	4680
GCCCGAGGA	CCACGCCGGA	CTTGCGCCT	TTCCTGGGTT	CCCAGTCTGC	CCGTGCTGTC	4740
TCGAAGCCGT	ACCGGCCCCC	CACGACTGCC	CGTTGGAAAG	AAGTCACCCC	GCTCCACGCG	4800
TGGAAGGGCG	TGACCGGAGA	CCGACCGGAA	GTCAGGGAGG	ACCCGGAGAC	AGCGGCGGTC	4860
GTCCAGGCTC	TGATCAGCGG	CCGTTATCCT	CAGAAGACGA	AGCTTCCCTC	CGACGCATCC	4920
AAAGGCTACT	CAAGAACTAA	GGG ATG CTC ACA ATC CAC CTC TTT TCC TGC				4970
Met Leu Thr Ile His Leu Phe Ser Cys						
1	5					
CCC GAG TGC GGA TTA CCA GGC CCG CGA CTG CCA GAC AGT CCG AGT CTG						5018
Pro Glu Cys Gly Leu Pro Gly Pro Arg Leu Pro Asp Ser Pro Ser Leu						
10	15	20	25			
CCG CGC CGC TGC AGA GAT GGC GCG CTC ATG TAT TCA CGA GCC GTT GGC						5066
Pro Arg Arg Cys Arg Asp Gly Ala Leu Met Tyr Ser Arg Ala Val Gly						
30	35	40				
TTC ATC TGC CGC CAG TGC CGA CTT GAA GCG CAT ACG CTC TAC CTC GGA						5114
Phe Ile Cys Arg Gln Cys Arg Leu Glu Ala His Thr Leu Tyr Leu Gly						
45	50	55				
CTC TGT TCC CGA TGT AAA GAT CAG CAA GAG CGC ATG AAG GAA CAA AAT						5162
Leu Cys Ser Arg Cys Lys Asp Gln Gln Glu Arg Met Lys Glu Gln Asn						
60	65	70				
TAGTTTCCTT GTTCGTAAAC AAGGTGGTCC CTCCCCATTGA GGTAAAGACT CTGGTGAGTC						5222
CTCAACGTTA CTCGTTGAGT CTGCTGCGGT TCGATTCCAT TCCCAAGCAG CAAAGGGTGC						5282
GCAACTAGTA CGGCGCCCCC TGGGATACCA						5312

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Leu Thr Ile His Leu Phe Ser Cys Pro Glu Cys Gly Leu Pro Gly						
1	5	10	15			
Pro Arg Leu Pro Asp Ser Pro Ser Leu Pro Arg Arg Cys Arg Asp Gly						
20	25	30				
Ala Leu Met Tyr Ser Arg Ala Val Gly Phe Ile Cys Arg Gln Cys Arg						
35	40	45				
Leu Glu Ala His Thr Leu Tyr Leu Gly Leu Cys Ser Arg Cys Lys Asp						
50	55	60				
Gln Gln Glu Arg Met Lys Glu Gln Asn						
65	70					

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 283..753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GTTCACCAAG TGTGGTAAAA TTTAACAAA GAAGAAACC AGGACCGTAA

60

CCCGGCCCTT	ACACACCTCG	AGTCCGTGAC	CACCGGATTA	TACGTCGCC	ACCACACGGC	120	
GCCTTTCCG	ACCACTCTCG	AGAGTCGTTG	GGAGTTTCGT	CCGTGACCCAC	CCGGTTGGCA	180	
GTCGACAGAC	GCTTCGGAC	CACTAGAAC	TCCTCGAGCG	ACGCACACAC	AGCACACACA	240	
CCGCCTTAGC	TGCACCTACG	GCAGCGTTGA	TAGCGCGGAT	TT ATG AGC GAG CAC		294	
				Met Ser Glu His			
				1			
ACC ATC	GCC CAC	TCC ATC	ACA TTA	CCA CCC	GGT TAC ACC	CTT GCC CTA	342
Thr Ile	Ala His	Ser Ile	Thr Leu	Pro Pro	Gly Tyr	Thr Leu Ala Leu	
5		10		15		20	
ATA CCC CCT	GAA CCT	GAA GCA	GGA TGG	GAG ATG	CTG GAG	TGG CGT CAC	390
Ile Pro Pro	Glu Pro	Glu Ala	Gly Trp	Glu Met	Leu Glu	Trp Arg His	
25		30		35			
AGC GAC CTC	ACA ACC GTC	GCG GAA	CCC GTA	ACG TTC	GGG TCA	GCG CCA	438
Ser Asp Leu	Thr Thr Val	Ala Glu	Pro Val	Thr Phe	Gly Ser	Ala Pro	
40		45		50			
ACA CCG TCA	CCG TCA	ATG GTA	GAA GAA	ACC AAC	GGC GTC	GGA CCG GAA	486
Thr Pro Ser	Pro Ser Met	Val Glu	Glu Thr	Asn Gly	Val Gly	Pro Glu	
55		60		65			
GGC AAG TTT	CTC CCC CTG	ACA ATT	TCA CCG	CTG CTG	CAC AAG	ACC TCG	534
Gly Lys Phe	Leu Pro	Leu Thr	Ile Ser	Pro Leu	Leu His	Lys Thr Ser	
70		75		80			
CGC AAA GCC TTG	ACG CCA ACA	CCG TCA	CTT TCC	CCG CTA	ACA TCT	CTA	582
Arg Lys Ala	Leu Thr Pro	Thr Pro Ser	Leu Ser	Pro Leu	Thr Ser	Leu	
85		90		95		100	
GCA TGC CCG AAT	TCC GGA ATT	GGG CCA	AGG GAA	AGA TCG	ACC TCG	ACT	630
Ala Cys Pro Asn	Ser Gly Ile	Gly Pro	Arg Glu	Arg Ser	Thr Ser	Thr	
105		110		115			
CCG ATT CCA TCG	GCT GGT ACT	TCA AGT	ACC TTG	ACC CAG	CGG GTG	CTA	678
Pro Ile Pro Ser	Ala Gly Thr	Ser Ser	Thr Thr	Leu Thr	Gln Arg	Val Leu	
120		125		130			
CAG AGT CTG CGC	GCG CCG TCG	GCG AGT	ACT CGA	AGA TCC	CTG ACG	GCC	726
Gln Ser Leu Arg	Ala Pro Ser	Ala Ser	Thr Arg	Arg Ser	Leu Thr	Ala	
135		140		145			
TCG TCA AGT TCT	CCG TCG	ACG CAG	AGA TAAGAGAGAT	CTATAACGAG			773
Ser Ser Ser Pro	Ser Thr Gln	Arg					
150		155					
GAGTGCCCCG	TCGTCACTGA	CGTGTCCGTC	CCCCTCGACG	GCCGCCAGTG	GAGCCTCTCG		833
ATTTCCTCCT	TTCCGATGTT	CAGAACCGCC	TACGTCGCC	TAGCGAACGT	CGAGAACAAAG		893
GAGATGTCGC	TCGACGTTGT	CAACGACCTC	ATCGAGTGGC	TCAACAAATCT	CGCCGACTGG		953
CGTTATGTCG	TTGACTCTGA	ACAGTGGATT	AACTTCACCA	ATGACACCCAC	GTACTACGTC		1013
CGCATCCCG	TTCTACGTCC	AACCTACGAC	GTTCCAGACC	CCACAGAGGG	CCTTGTTCGC		1073
ACAGTCTCAG	ACTACCGCCT	CACTTATAAG	GCGATAAACAT	GTGAAGCCAA	CATGCCAACAA		1133
CTCGTCGACC	AAGGCTTTG	GATCGGCGGC	CAGTACGCTC	TCACCCCGAC	TAGCCTACCG		1193
CAGTACGACG	TCAGCGAGGC	CTACGCTCTG	CACACTTGA	CCTTCGCCAG	ACCATCCAGC		1253
GCCGCTGCAC	TCGCCTTGT	GTGGGCAGGT	TTGCCACAGG	GTGGCACTGC	GCCTGCAGGC		1313
ACTCCAGCCT	GGGAGCAGGC	ATCCTCGGGT	GGCTACCTCA	CCTGGCGCCA	CAACGGTACT		1373
ACTTCCCAG	CTGGCTCCGT	TAGCTACGTT	CTCCCTGAGG	GTTCGCCCC	TGAGCGCTAC		1433
GACCCGAACG	ACGGCTCTTG	GACCGACTTC	GCTTCGCCAG	GAGACACCGT	CACTTCCGG		1493
CAGGTCGCCG	TCGACGAGGT	CGTTGTGACC	AACAAACCCCG	CCGGCGGCCGG	CAGCGCCCCC		1553
ACCTTCACCG	TGAGAGTGCC	CCCTTCAAAC	GCTTACACCA	ACACCGTGT	TAGGAACACG		1613
CTCTTAGAGA	CTCGACCCCTC	CTCTCGTAGG	CTCGAACTCC	CTATGCCACC	TGCTGACTTT		1673
GGACAGACGG	TCGCCAACAA	CCCGAAGATC	GAGCAGTCGC	TTCTTAAAGA	AACACTTGGC		1733
TGCTATTTGG	TCCACTCCAA	AATGCGAAC	CCCGTTTTCC	AGCTCACGCC	AGCCAGCTCC		1793
TTTGGCGCCG	TTTCCTTCAA	CAATCCGGGT	TATGAGCGCA	CACCGACCT	CCCGGACTAC		1853
ACTGGCATTCC	GTGACTCATT	CGACCAGAAC	ATGTCCACCG	CTGTGGCCA	CTTCCGCTCA		1913
CTCTCCCACT	CCTGCAGTAT	CGTCACTAAG	ACCTACCAGG	GTGGGAAAGG	CGTCACGAAC		1973
GTCAACACGC	CTTTCGGCCA	ATTCGCGCAC	GCGGGCCTCC	TCAAGAATGA	GGAGATCCTC		2033

TGCCTCGCCG	ACGACCTGGC	CACCCGTCTC	ACAGGTGTCT	ACCCCGCCAC	TGACAACATT	2093
GCGGCCGCCG	TTTCTGCCTT	CGCCCGAAC	ATGCTGTCT	CCGTGCTGAA	GTCCGGAGGCA	2153
ACGTCCCTCCA	TCATCAAGTC	CGTTGGCGAG	ACTGCCGTG	GCGCGGCTCA	GTCCGGCCTC	2213
GCGAAGCTAC	CCGGACTGCT	AATGAGTGT	CCAGGGAAGA	TTGCCGCGCG	TGTCCGCGCG	2273
CGCCGAGCGC	GCCGCCGCGC	CGCTCGTGC	AATTAGTTG	CTCGCTCTG	TTTCGCCGTT	2333
TCGTAAAACG	GCGTGGTCCC	GCACATTACG	CGTACCCCTAA	AGACTCTGGT	GAGTCCCCGT	2393
C GTTACACGA	CGGGCTGCGC	GCGGTTCGAT	TCCATTCCCA	AGCGGCAAGA	AGGACGTAGT	2453
TAGCTCTGCG	TCCCTCGGG	TACCA				2478

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Met Ser Glu His Thr Ile Ala His Ser Ile Thr Leu Pro Pro Gly Tyr
1           5           10          15
Thr Leu Ala Leu Ile Pro Pro Glu Pro Ala Gly Trp Glu Met Leu
20          25          30
Glu Trp Arg His Ser Asp Leu Thr Thr Val Ala Glu Pro Val Thr Phe
35          40          45
Gly Ser Ala Pro Thr Pro Ser Pro Ser Met Val Glu Glu Thr Asn Gly
50          55          60
Val Gly Pro Glu Gly Lys Phe Leu Pro Leu Thr Ile Ser Pro Leu Leu
65          70          75          80
His Lys Thr Ser Arg Lys Ala Leu Thr Pro Thr Pro Ser Leu Ser Pro
85          90          95
Leu Thr Ser Leu Ala Cys Pro Asn Ser Gly Ile Gly Pro Arg Glu Arg
100         105         110
Ser Thr Ser Thr Pro Ile Pro Ser Ala Gly Thr Ser Ser Thr Leu Thr
115         120         125
Gln Arg Val Leu Gln Ser Leu Arg Ala Pro Ser Ala Ser Thr Arg Arg
130         135         140
Ser Leu Thr Ala Ser Ser Ser Pro Ser Thr Gln Arg
145         150         155

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(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 366..2306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GT TTTCTTT	CTTTACCAAG	TGTGGTAAAA	TTTAAACAAA	GAAGAAAACC	AGGACCGTAA	60
CCCGGCCCTT	ACACACCTCG	AGTCCGTGAC	CACCGGATTA	TACGTGCC	ACCACACGGC	120
GCC TTTCCG	ACCACTCTCG	AGAGTCGTTG	GGAGTTTCGT	CCGTGACCAC	CCGGTTGGCA	180
GTCGACAGAC	GCTCCGGAC	CACTAGAAC	TCCTCGAGCG	ACGCACACAC	AGCACACACA	240
CCGCCTTAGC	TGCACCTACG	GCAGCGTTGA	TAGCGGGAT	TTATGAGCGA	GCACACCATC	300
GCCCACCTCCA	TCACATTACC	ACCCGGTTAC	ACCCTGCC	TAATACCCCC	TGAACCTGAA	360

GCAGG ATG GGA GAT GCT GGA GTG GCG TCA CAG CGA CCT CAC AAC CGT	407
Met Gly Asp Ala Gly Val Ala Ser Gln Arg Pro His Asn Arg	
1 5 10	
CGC GGA ACC CGT AAC GTT CGG GTC AGC GCC AAC ACC GTC ACC GTC AAT	455
Arg Gly Thr Arg Asn Val Arg Val Ser Ala Asn Thr Val Thr Val Asn	
15 20 25 30	
GGT AGA AGA AAC CAA CGG CGT CGG ACC GGA AGG CAA GTT TCT CCC CCT	503
Gly Arg Arg Asn Gln Arg Arg Arg Thr Gly Arg Gln Val Ser Pro Pro	
35 40 45	
GAC AAT TTC ACC GCT GCA CAA GAC CTC GCG CAA AGC CTT GAC GCC	551
Asp Asn Phe Thr Ala Ala Gln Asp Leu Ala Gln Ser Leu Asp Ala	
50 55 60	
AAC ACC GTC ACT TTC CCC GCT AAC ATC TCT AGC ATG CCC GAA TTC CGG	599
Asn Thr Val Thr Phe Pro Ala Asn Ile Ser Ser Met Pro Glu Phe Arg	
65 70 75	
AAT TGG GCC AAG GGA AAG ATC GAC CTC GAC TCC GAT TCC ATC GGC TGG	647
Asn Trp Ala Lys Gly Lys Ile Asp Leu Asp Ser Asp Ser Ile Gly Trp	
80 85 90	
TAC TTC AAG TAC CTT GAC CCA GCG GGT GCT ACA GAG TCT GCG CGC GCC	695
Tyr Phe Lys Tyr Leu Asp Pro Ala Gly Ala Thr Glu Ser Ala Arg Ala	
95 100 105 110	
GTC GGC GAG TAC TCG AAG ATC CCT GAC GGC CTC GTC AAG TTC TCC GTC	743
Val Gly Glu Tyr Ser Lys Ile Pro Asp Gly Leu Val Lys Phe Ser Val	
115 120 125	
GAC GCA GAG ATA AGA GAG ATC TAT AAC GAG GAG TGC CCC GTC GTC ACT	791
Asp Ala Glu Ile Arg Glu Ile Tyr Asn Glu Glu Cys Pro Val Val Thr	
130 135 140	
GAC GTG TCC GTC CCC CTC GAC GGC CGC CAG TGG AGC CTC TCG ATT TTC	839
Asp Val Ser Val Pro Leu Asp Gly Arg Gln Trp Ser Leu Ser Ile Phe	
145 150 155	
TCC TTT CCG ATG TTC AGA ACC GCC TAC GTC GCC GTA GCG AAC GTC GAG	887
Ser Phe Pro Met Phe Arg Thr Ala Tyr Val Ala Val Ala Asn Val Glu	
160 165 170	
AAC AAG GAG ATG TCG CTC GAC GTT GTC AAC GAC CTC ATC GAG TGG CTC	935
Asn Lys Glu Met Ser Leu Asp Val Val Asn Asp Leu Ile Glu Trp Leu	
175 180 185 190	
AAC AAT CTC GCC GAC TGG CGT TAT GTC GTT GAC TCT GAA CAG TGG ATT	983
Asn Asn Leu Ala Asp Trp Arg Tyr Val Val Asp Ser Glu Gln Trp Ile	
195 200 205	
AAC TTC ACC AAT GAC ACC ACG TAC TAC GTC CGC ATC CGC GTT CTA CGT	1031
Asn Phe Thr Asn Asp Thr Thr Tyr Val Arg Ile Arg Val Leu Arg	
210 215 220	
CCA ACC TAC GAC GTT CCA GAC CCC ACA GAG GGC CTT GTT CGC ACA GTC	1079
Pro Thr Tyr Asp Val Pro Asp Pro Thr Glu Gly Leu Val Arg Thr Val	
225 230 235	
TCA GAC TAC CGC CTC ACT TAT AAG GCG ATA ACA TGT GAA GCC AAC ATG	1127
Ser Asp Tyr Arg Leu Thr Tyr Lys Ala Ile Thr Cys Glu Ala Asn Met	
240 245 250	
CCA ACA CTC GTC GAC CAA GGC TTT TGG ATC GGC GGC CAG TAC GCT CTC	1175
Pro Thr Leu Val Asp Gln Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu	
255 260 265 270	
ACC CCG ACT AGC CTA CCG CAG TAC GAC GTC AGC GAG GCC TAC GCT CTG	1223
Thr Pro Thr Ser Leu Pro Gln Tyr Asp Val Ser Glu Ala Tyr Ala Leu	
275 280 285	
CAC ACT TTG ACC TTC GCC AGA CCA TCC AGC GCC GCT GCA CTC GCG TTT	1271
His Thr Leu Thr Phe Ala Arg Pro Ser Ser Ala Ala Ala Leu Ala Phe	
290 295 300	

GTG TGG GCA GGT TTG CCA CAG GGT GGC ACT GCG CCT GCA GGC ACT CCA	1319
Val Trp Ala Gly Leu Pro Gln Gly Gly Thr Ala Pro Ala Gly Thr Pro	
305 310 315	
GCC TGG GAG CAG GCA TCC TCG GGT GGC TAC CTC ACC TGG CGC CAC AAC	1367
Ala Trp Glu Gln Ala Ser Ser Gly Gly Tyr Leu Thr Trp Arg His Asn	
320 325 330	
GGT ACT ACT TTC CCA GCT GGC TCC GTT AGC TAC GTT CTC CCT GAG GGT	1415
Gly Thr Thr Phe Pro Ala Gly Ser Val Ser Tyr Val Leu Pro Glu Gly	
335 340 345 350	
TTC GCC CTT GAG CGC TAC GAC CCG AAC GAC GGC TCT TGG ACC GAC TTC	1463
Phe Ala Leu Glu Arg Tyr Asp Pro Asn Asp Gly Ser Trp Thr Asp Phe	
355 360 365	
GCT TCC GCA GGA GAC ACC GTC ACT TTC CGG CAG GTC GCC GTC GAC GAG	1511
Ala Ser Ala Gly Asp Thr Val Thr Phe Arg Gln Val Ala Val Asp Glu	
370 375 380	
GTC GTT GTG ACC AAC AAC CCC GCC GGC GGC GGC AGC GCC CCC ACC TTC	1559
Val Val Val Thr Asn Asn Pro Ala Gly Gly Ser Ala Pro Thr Phe	
385 390 395	
ACC GTG AGA GTG CCC CCT TCA AAC GCT TAC ACC AAC ACC GTG TTT AGG	1607
Thr Val Arg Val Pro Pro Ser Asn Ala Tyr Thr Asn Thr Val Phe Arg	
400 405 410	
AAC ACG CTC TTA GAG ACT CGA CCC TCC TCT CGT AGG CTC GAA CTC CCT	1655
Asn Thr Leu Leu Glu Thr Arg Pro Ser Ser Arg Arg Leu Glu Leu Pro	
415 420 425 430	
ATG CCA CCT GCT GAC TTT GGA CAG ACG GTC GCC AAC AAC CCG AAG ATC	1703
Met Pro Pro Ala Asp Phe Gly Gln Thr Val Ala Asn Asn Pro Lys Ile	
435 440 445	
GAG CAG TCG CTT CTT AAA GAA ACA CTT GGC TGC TAT TTG GTC CAC TCC	1751
Glu Gln Ser Leu Leu Lys Glu Thr Leu Gly Cys Tyr Leu Val His Ser	
450 455 460	
AAA ATG CGA AAC CCC GTT TTC CAG CTC ACG CCA GCC AGC TCC TTT GGC	1799
Lys Met Arg Asn Pro Val Phe Gln Leu Thr Pro Ala Ser Ser Phe Gly	
465 470 475	
GCC GTT TCC TTC AAC AAT CCG GGT TAT GAG CGC ACA CGC GAC CTC CCG	1847
Ala Val Ser Phe Asn Asn Pro Gly Tyr Glu Arg Thr Arg Asp Leu Pro	
480 485 490	
GAC TAC ACT GGC ATC CGT GAC TCA TTC GAC CAG AAC ATG TCC ACC GCT	1895
Asp Tyr Thr Gly Ile Arg Asp Ser Phe Asp Gln Asn Met Ser Thr Ala	
495 500 505 510	
GTG GCC CAC TTC CGC TCA CTC TCC CAC TCC TGC AGT ATC GTC ACT AAG	1943
Val Ala His Phe Arg Ser Leu Ser His Ser Cys Ser Ile Val Thr Lys	
515 520 525	
ACC TAC CAG GGT TGG GAA GGC GTC ACG AAC GTC AAC ACG CCT TTC GGC	1991
Thr Tyr Gln Gly Trp Glu Gly Val Thr Asn Val Asn Thr Pro Phe Gly	
530 535 540	
CAA TTC GCG CAC GCG GGC CTC CTC AAG AAT GAG GAG ATC CTC TGC CTC	2039
Gln Phe Ala His Ala Gly Leu Leu Lys Asn Glu Glu Ile Leu Cys Leu	
545 550 555	
GCC GAC GAC CTG GCC ACC CGT CTC ACA GGT GTC TAC CCC GCC ACT GAC	2087
Ala Asp Asp Leu Ala Thr Arg Leu Thr Gly Val Tyr Pro Ala Thr Asp	
560 565 570	
AAC TTC GCG GCC GCC GTT TCT GCC TTC GCG AAC ATG CTG TCC TCC	2135
Asn Phe Ala Ala Ala Val Ser Ala Phe Ala Ala Asn Met Leu Ser Ser	
575 580 585 590	
GTG CTG AAG TCG GAG GCA ACG TCC TCC ATC ATC AAG TCC GTT GGC GAG	2183
Val Leu Lys Ser Glu Ala Thr Ser Ser Ile Ile Lys Ser Val Gly Glu	
595 600 605	

ACT GCC GTC GGC GCG GCT CAG TCC GGC CTC GCG AAG CTA CCC GGA CTG	2231
Thr Ala Val Gly Ala Ala Gln Ser Gly Leu Ala Lys Leu Pro Gly Leu	
610 615 620	
CTA ATG AGT GTA CCA GGG AAG ATT GCC GCG CGT GTC CGC GCG CGC CGA	2279
Leu Met Ser Val Pro Gly Lys Ile Ala Ala Arg Val Arg Ala Arg Arg	
625 630 635	
GCG CGC CGC CGC GCC GCT CGT GCC AAT TAGTTGCTC GCTCCTGTTT	2326
Ala Arg Arg Arg Ala Ala Arg Ala Asn	
640 645	
CGCCGTTTCG TAAAACGGCG TGGTCCCAGCA CATTACGCGT ACCCTAAAGA CTCTGGTGAG	2386
TCCCCGTCGT TACACGACGG GTCTGCCGCG GTTCGATTCC ATTCCCAAGC GGCAAGAAGG	2446
ACGTAGTTAG CTCTGCGTCC CTCGGGATAC CA	2478

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 647 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Asp Ala Gly Val Ala Ser Gln Arg Pro His Asn Arg Arg Gly
 1 5 10 15

Thr Arg Asn Val Arg Val Ser Ala Asn Thr Val Thr Val Asn Gly Arg
 20 25 30

Arg Asn Gln Arg Arg Arg Thr Gly Arg Gln Val Ser Pro Pro Asp Asn
 35 40 45

Phe Thr Ala Ala Ala Gln Asp Leu Ala Gln Ser Leu Asp Ala Asn Thr
 50 55 60

Val Thr Phe Pro Ala Asn Ile Ser Ser Met Pro Glu Phe Arg Asn Trp
 65 70 75 80

Ala Lys Gly Lys Ile Asp Leu Asp Ser Asp Ser Ile Gly Trp Tyr Phe
 85 90 95

Lys Tyr Leu Asp Pro Ala Gly Ala Thr Glu Ser Ala Arg Ala Val Gly
 100 105 110

Glu Tyr Ser Lys Ile Pro Asp Gly Leu Val Lys Phe Ser Val Asp Ala
 115 120 125

Glu Ile Arg Glu Ile Tyr Asn Glu Glu Cys Pro Val Val Thr Asp Val
 130 135 140

Ser Val Pro Leu Asp Gly Arg Gln Trp Ser Leu Ser Ile Phe Ser Phe
 145 150 155 160

Pro Met Phe Arg Thr Ala Tyr Val Ala Val Ala Asn Val Glu Asn Lys
 165 170 175

Glu Met Ser Leu Asp Val Val Asn Asp Leu Ile Glu Trp Leu Asn Asn
 180 185 190

Leu Ala Asp Trp Arg Tyr Val Val Asp Ser Glu Gln Trp Ile Asn Phe
 195 200 205

Thr Asn Asp Thr Thr Tyr Tyr Val Arg Ile Arg Val Leu Arg Pro Thr
 210 215 220

Tyr Asp Val Pro Asp Pro Thr Glu Gly Leu Val Arg Thr Val Ser Asp
 225 230 235 240

Tyr Arg Leu Thr Tyr Lys Ala Ile Thr Cys Glu Ala Asn Met Pro Thr
 245 250 255

Leu Val Asp Gln Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu Thr Pro
 260 265 270

Thr Ser Leu Pro Gln Tyr Asp Val Ser Glu Ala Tyr Ala Leu His Thr
 275 280 285

Leu Thr Phe Ala Arg Pro Ser Ser Ala Ala Ala Leu Ala Phe Val Trp
 290 295 300
 Ala Gly Leu Pro Gln Gly Gly Thr Ala Pro Ala Gly Thr Pro Ala Trp
 305 310 315 320
 Glu Gln Ala Ser Ser Gly Gly Tyr Leu Thr Trp Arg His Asn Gly Thr
 325 330 335
 Thr Phe Pro Ala Gly Ser Val Ser Tyr Val Leu Pro Glu Gly Phe Ala
 340 345 350
 Leu Glu Arg Tyr Asp Pro Asn Asp Gly Ser Trp Thr Asp Phe Ala Ser
 355 360 365
 Ala Gly Asp Thr Val Thr Phe Arg Gln Val Ala Val Asp Glu Val Val
 370 375 380
 Val Thr Asn Asn Pro Ala Gly Gly Ser Ala Pro Thr Phe Thr Val
 385 390 395 400
 Arg Val Pro Pro Ser Asn Ala Tyr Thr Asn Thr Val Phe Arg Asn Thr
 405 410 415
 Leu Leu Glu Thr Arg Pro Ser Ser Arg Arg Leu Glu Leu Pro Met Pro
 420 425 430
 Pro Ala Asp Phe Gly Gln Thr Val Ala Asn Asn Pro Lys Ile Glu Gln
 435 440 445
 Ser Leu Leu Lys Glu Thr Leu Gly Cys Tyr Leu Val His Ser Lys Met
 450 455 460
 Arg Asn Pro Val Phe Gln Leu Thr Pro Ala Ser Ser Phe Gly Ala Val
 465 470 475 480
 Ser Phe Asn Asn Pro Gly Tyr Glu Arg Thr Arg Asp Leu Pro Asp Tyr
 485 490 495
 Thr Gly Ile Arg Asp Ser Phe Asp Gln Asn Met Ser Thr Ala Val Ala
 500 505 510
 His Phe Arg Ser Leu Ser His Ser Cys Ser Ile Val Thr Lys Thr Tyr
 515 520 525
 Gln Gly Trp Glu Gly Val Thr Asn Val Asn Thr Pro Phe Gly Gln Phe
 530 535 540
 Ala His Ala Gly Leu Leu Lys Asn Glu Glu Ile Leu Cys Leu Ala Asp
 545 550 555 560
 Asp Leu Ala Thr Arg Leu Thr Gly Val Tyr Pro Ala Thr Asp Asn Phe
 565 570 575
 Ala Ala Ala Val Ser Ala Phe Ala Ala Asn Met Leu Ser Ser Val Leu
 580 585 590
 Lys Ser Glu Ala Thr Ser Ser Ile Ile Lys Ser Val Gly Glu Thr Ala
 595 600 605
 Val Gly Ala Ala Gln Ser Gly Leu Ala Lys Leu Pro Gly Leu Leu Met
 610 615 620
 Ser Val Pro Gly Lys Ile Ala Ala Arg Val Arg Ala Arg Arg Ala Arg
 625 630 635 640
 Arg Arg Ala Ala Arg Ala Asn
 645

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 283..2307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GT	TTT	TCT	TTT	ACCAAG	TGTGGT	AAAAA	TTTAA	ACAAA	GAAGAAA	ACC	AGGACCG	TAA	60			
CC	GG	CCC	TTT	ACACAC	CTCG	AGTCCG	TGAC	CACCGG	ATTA	TACGTC	GCCC	ACCACAC	GGC	120		
GC	CTT	TTT	CCG	CC	ACTCTCG	AGAGTC	GTTG	GGAGT	TTCGT	CCGTG	ACCCAC	CCGGT	TTGGCA	180		
GTC	GAC	AGAC	GCT	TCCGGAC	CACTAGAA	ACC	TCC	TGAGCG	ACCGCAC	ACAC	AGCACACACA	240				
CCG	CCT	TTA	AGC	TAGCCTACG	GCAGCG	TTG	ATG	AGC	GAG	CAC	Met	Ser	Glu	294		
														1		
ACC	ATC	GCC	CAC	TCC	ATC	ACA	TTA	CCA	CCC	GGT	TAC	ACC	CTT	GCC	CTA	342
Thr	Ile	Ala	His	His	Ile	Thr	Leu	Pro	Pro	Gly	Tyr	Thr	Leu	Ala	Leu	
5						10				15				20		
ATA	CCC	CCT	GAA	CCT	GAA	GCA	GGG	TGG	GAG	ATG	CTG	GAG	TGG	CGT	CAC	390
Ile	Pro	Pro	Glu	Pro	Glu	Ala	Gly	Trp	Glu	Met	Leu	Glu	Trp	Arg	His	
						25			30				35			
AGC	GAC	CTC	ACA	ACC	GTC	GCG	GAA	CCC	GTA	ACG	TTC	GGG	TCA	GCG	CCA	438
Ser	Asp	Leu	Thr	Thr	Val	Ala	Glu	Pro	Val	Thr	Phe	Gly	Ser	Ala	Pro	
						40			45			50				
ACA	CCG	TCA	CCG	TCA	ATG	GTA	GAA	GAA	ACC	AAC	GGC	GTC	GGA	CCG	GAA	486
Thr	Pro	Ser	Pro	Ser	Met	Val	Glu	Glu	Thr	Asn	Gly	Val	Gly	Pro	Glu	
						55			60			65				
GGC	AAG	TTT	CTC	CCC	CTG	ACA	ATT	TCA	CCG	CTG	CTG	CAC	AAG	ACC	TCG	534
Gly	Lys	Phe	Leu	Pro	Leu	Thr	Ile	Ser	Pro	Leu	Leu	His	Lys	Thr	Ser	
						70			75			80				
CGC	AAA	GCC	TTG	ACG	CCA	ACA	CCG	TCA	CTT	TCC	CCC	GCT	AAC	ATC	TCT	582
Arg	Lys	Ala	Leu	Thr	Pro	Thr	Pro	Ser	Leu	Ser	Pro	Ala	Asn	Ile	Ser	
						85			90			95			100	
AGC	ATG	CCC	GAA	TTC	CGG	AAT	TGG	GCC	AAG	GGA	AAG	ATC	GAC	CTC	GAC	630
Ser	Met	Pro	Glu	Phe	Arg	Asn	Trp	Ala	Lys	Gly	Lys	Ile	Asp	Leu	Asp	
						105			110			115				
TCC	GAT	TCC	ATC	GGC	TGG	TAC	TTC	AAG	TAC	CTT	GAC	CCA	GCG	GGT	GCT	678
Ser	Asp	Ser	Ile	Gly	Trp	Tyr	Phe	Lys	Tyr	Leu	Asp	Pro	Ala	Gly	Ala	
						120			125			130				
ACA	GAG	TCT	GCG	CGC	GCC	GTC	GGC	GAG	TAC	TCG	AAG	ATC	CCT	GAC	GGC	726
Thr	Glu	Ser	Ala	Arg	Ala	Val	Gly	Glu	Tyr	Ser	Lys	Ile	Pro	Asp	Gly	
						135			140			145				
CTC	GTC	AAG	TTC	TCC	GTC	GAC	GCA	GAG	ATA	AGA	GAG	ATC	TAT	AAC	GAG	774
Leu	Val	Lys	Phe	Ser	Val	Asp	Ala	Glu	Ile	Arg	Glu	Ile	Tyr	Asn	Glu	
						150			155			160				
GAG	TGC	CCC	GTC	GTC	ACT	GAC	GTG	TCC	GTC	CCC	CTC	GAC	GGC	CGC	CAG	822
Glu	Cys	Pro	Val	Val	Thr	Asp	Val	Ser	Val	Pro	Leu	Asp	Gly	Arg	Gln	
						165			170			175			180	
TGG	AGC	CTC	TCG	ATT	TTC	TCC	TTT	CCG	ATG	TTC	AGA	ACC	GCC	TAC	GTC	870
Trp	Ser	Leu	Ser	Ile	Phe	Ser	Phe	Pro	Met	Phe	Arg	Thr	Ala	Tyr	Val	
						185			190			195				
GCC	GTA	GCG	AAC	GTC	GAG	AAC	AAG	GAG	ATG	TCG	CTC	GAC	GTT	GTC	AAC	918
Ala	Val	Ala	Asn	Val	Glu	Asn	Lys	Glu	Met	Ser	Leu	Asp	Val	Val	Asn	
						200			205			210				
GAC	CTC	ATC	GAG	TGG	CTC	AAC	AAT	CTC	GCC	GAC	TGG	CGT	TAT	GTC	GTT	966
Asp	Leu	Ile	Glu	Trp	Leu	Asn	Asn	Leu	Ala	Asp	Trp	Arg	Tyr	Val	Val	
						215			220			225				
GAC	TCT	GAA	CAG	TGG	ATT	AAC	TTC	ACC	AAT	GAC	ACC	ACG	TAC	TAC	GTC	1014
Asp	Ser	Glu	Gln	Trp	Ile	Asn	Phe	Thr	Asn	Asp	Thr	Thr	Tyr	Tyr	Val	
						230			235			240				
CGC	ATC	CGC	GTT	CTA	CGT	CCA	ACC	TAC	GAC	GTT	CCA	GAC	CCC	ACA	GAG	1062
Arg	Ile	Arg	Val	Leu	Arg	Pro	Thr	Tyr	Asp	Val	Pro	Asp	Pro	Thr	Glu	

245	250	255	260	
Gly CTT GTT CGC ACA GTC TCA GAC TAC CGC CTC ACT TAT AAG GCG ATA				1110
Gly Leu Val Arg Thr Val Ser Asp Tyr Arg Leu Thr Tyr Lys Ala Ile				
265	270	275		
ACA TGT GAA GCC AAC ATG CCA ACA CTC GTC GAC CAA GGC TTT TGG ATC				1158
Thr Cys Glu Ala Asn Met Pro Thr Leu Val Asp Gln Gly Phe Trp Ile				
280	285	290		
Gly GGC CAG TAC GCT CTC ACC CCG ACT AGC CTA CCG CAG TAC GAC GTC				1206
Gly Gly Gln Tyr Ala Leu Thr Pro Thr Ser Leu Pro Gln Tyr Asp Val				
295	300	305		
AGC GAG GCC TAC GCT CTG CAC ACT TTG ACC TTC GCC AGA CCA TCC AGC				1254
Ser Glu Ala Tyr Ala Leu His Thr Leu Thr Phe Ala Arg Pro Ser Ser				
310	315	320		
GCC GCT GCA CTC GCG TTT GTG TGG GCA GGT TTG CCA CAG GGT GGC ACT				1302
Ala Ala Ala Leu Ala Phe Val Trp Ala Gly Leu Pro Gln Gly Thr				
325	330	335	340	
GCG CCT GCA GGC ACT CCA GCC TGG GAG CAG GCA TCC TCG GGT GGC TAC				1350
Ala Pro Ala Gly Thr Pro Ala Trp Glu Gln Ala Ser Ser Gly Gly Tyr				
345	350	355		
CTC ACC TGG CGC CAC AAC GGT ACT ACT TTC CCA GCT GGC TCC GTT AGC				1398
Leu Thr Trp Arg His Asn Gly Thr Thr Phe Pro Ala Gly Ser Val Ser				
360	365	370		
TAC GTT CTC CCT GAG GGT TTC GCC CTT GAG CGC TAC GAC CCG AAC GAC				1446
Tyr Val Leu Pro Glu Gly Phe Ala Leu Glu Arg Tyr Asp Pro Asn Asp				
375	380	385		
GCG TCT TGG ACC GAC TTC GCT TCC GCA GGA GAC ACC GTC ACT TTC CGG				1494
Gly Ser Trp Thr Asp Phe Ala Ser Ala Gly Asp Thr Val Thr Phe Arg				
390	395	400		
CAG GTC GCC GTC GAC GAG GTC GTT GTG ACC AAC AAC CCC GCC GGC GGC				1542
Gln Val Ala Val Asp Glu Val Val Val Thr Asn Asn Pro Ala Gly Gly				
405	410	415	420	
GGC AGC GCC CCC ACC TTC ACC GTG AGA GTG CCC CCT TCA AAC GCT TAC				1590
Gly Ser Ala Pro Thr Phe Thr Val Arg Val Pro Pro Ser Asn Ala Tyr				
425	430	435		
ACC AAC ACC GTG TTT AGG AAC ACG CTC TTA GAG ACT CGA CCC TCC TCT				1638
Thr Asn Thr Val Phe Arg Asn Thr Leu Leu Glu Thr Arg Pro Ser Ser				
440	445	450		
CGT AGG CTC GAA CTC CCT ATG CCA CCT GCT GAC TTT GGA CAG ACG GTC				1686
Arg Arg Leu Glu Leu Pro Met Pro Pro Ala Asp Phe Gly Gln Thr Val				
455	460	465		
GCC AAC AAC CCG AAG ATC GAG CAG TCG CTT CTT AAA GAA ACA CTT GGC				1734
Ala Asn Asn Pro Lys Ile Glu Gln Ser Leu Leu Lys Glu Thr Leu Gly				
470	475	480		
TGC TAT TTG GTC CAC TCC AAA ATG CGA AAC CCC GTT TTC CAG CTC ACG				1782
Cys Tyr Leu Val His Ser Lys Met Arg Asn Pro Val Phe Gln Leu Thr				
485	490	495	500	
CCA GCC AGC TCC TTT GGC GCC GTT TCC TTC AAC AAT CCG GGT TAT GAG				1830
Pro Ala Ser Ser Phe Gly Ala Val Ser Phe Asn Asn Pro Gly Tyr Glu				
505	510	515		
CGC ACA CGC GAC CTC CCG GAC TAC ACT GGC ATC CGT GAC TCA TTC GAC				1878
Arg Thr Arg Asp Leu Pro Asp Tyr Thr Gly Ile Arg Asp Ser Phe Asp				
520	525	530		
CAG AAC ATG TCC ACC GCT GTG GCC CAC TTC CGC TCA CTC TCC CAC TCC				1926
Gln Asn Met Ser Thr Ala Val Ala His Phe Arg Ser Leu Ser His Ser				
535	540	545		
TGC AGT ATC GTC ACT AAG ACC TAC CAG GGT TGG GAA GGC GTC ACG AAC				1974
Cys Ser Ile Val Thr Lys Thr Tyr Gln Gly Trp Glu Gly Val Thr Asn				

550	555	560		
GTC AAC ACG CCT TTC GGC CAA TTC GCG CAC GCG	GGC CTC CTC AAG AAT		2022	
Val Asn Thr Pro Phe Gly Gln Phe Ala His Ala	Gly Leu Leu Lys Asn			
565	570	575	580	
GAG GAG ATC CTC TGC CTC GCC GAC GAC CTG	GCC ACC CGT CTC ACA GGT		2070	
Glu Glu Ile Leu Cys Leu Ala Asp Asp Leu Ala	Thr Arg Leu Thr Gly			
585	590	595		
GTC TAC CCC GCC ACT GAC AAC TTC GCG GCC	GCC GTT TCT GCC TTC GCC		2118	
Val Tyr Pro Ala Thr Asp Asn Phe Ala Ala	Ala Val Ser Ala Phe Ala			
600	605	610		
GCG AAC ATG CTG TCC GTG CTG AAG TCG GAG	GCA ACG TCC TCC ATC		2166	
Ala Asn Met Leu Ser Ser Val Leu Lys Ser	Glu Ala Thr Ser Ser Ile			
615	620	625		
ATC AAG TCC GTT GGC GAG ACT GCC GTC GGC	GCG GCT CAG TCC GGC CTC		2214	
Ile Lys Ser Val Gly Glu Thr Ala Val Gly	Ala Ala Gln Ser Gly Leu			
630	635	640		
GCG AAG CTA CCC GGA CTG CTA ATG AGT GTA	CCA GGG AAG ATT GCC GCG		2262	
Ala Lys Leu Pro Gly Leu Leu Met Ser Val	Pro Gly Lys Ile Ala Ala			
645	650	655	660	
CGT GTC CGC GCG CGC CGA GCG CGC CGC	GCC GCT CGT GCC AAT		2307	
Arg Val Arg Ala Arg Arg Arg Ala Ala Arg	Ala Asn			
665	670	675		
TAGTTTGCTC GCTCCTGTTT CGCCGTTTCG TAAAACGGCG TGGTCCCGCA CATTACGCGT				2367
ACCCTAAAGA CTCTGGTGAG TCCCCGTCGT TACACGACGG GTCTGCCGCG GTTCGATTCC				2427
ATTCCCAAGC GGCAAGAAGG ACGTAGTTAG CTCTGCGTCC CTCGGGATAC CA				2479

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

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Met Ser Glu His Thr Ile Ala His Ser Ile Thr Leu Pro Pro Gly Tyr
 1           5           10          15
Thr Leu Ala Leu Ile Pro Pro Glu Pro Glu Ala Gly Trp Glu Met Leu
 20          25          30
Glu Trp Arg His Ser Asp Leu Thr Thr Val Ala Glu Pro Val Thr Phe
 35          40          45
Gly Ser Ala Pro Thr Pro Ser Pro Ser Met Val Glu Glu Thr Asn Gly
 50          55          60
Val Gly Pro Glu Gly Lys Phe Leu Pro Leu Thr Ile Ser Pro Leu Leu
 65          70          75          80
His Lys Thr Ser Arg Lys Ala Leu Thr Pro Thr Pro Ser Leu Ser Pro
 85          90          95
Ala Asn Ile Ser Ser Met Pro Glu Phe Arg Asn Trp Ala Lys Gly Lys
100         105         110
Ile Asp Leu Asp Ser Asp Ser Ile Gly Trp Tyr Phe Lys Tyr Leu Asp
115         120         125
Pro Ala Gly Ala Thr Glu Ser Ala Arg Ala Val Gly Glu Tyr Ser Lys
130         135         140
Ile Pro Asp Gly Leu Val Lys Phe Ser Val Asp Ala Glu Ile Arg Glu
145         150         155         160
Ile Tyr Asn Glu Glu Cys Pro Val Val Thr Asp Val Ser Val Pro Leu
165         170         175
Asp Gly Arg Gln Trp Ser Leu Ser Ile Phe Ser Phe Pro Met Phe Arg

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180	185	190
Thr Ala Tyr Val Ala Val Ala Asn Val Glu Asn Lys	Glu Met Ser Leu	
195	200	205
Asp Val Val Asn Asp Leu Ile Glu Trp. Leu Asn Asn Leu Ala Asp Trp		
210	215	220
Arg Tyr Val Val Asp Ser Glu Gln Trp Ile Asn Phe Thr Asn Asp Thr		
225	230	235
Thr Tyr Tyr Val Arg Ile Arg Val Leu Arg Pro Thr Tyr Asp Val Pro		
245	250	255
Asp Pro Thr Glu Gly Leu Val Arg Thr Val Ser Asp Tyr Arg Leu Thr		
260	265	270
Tyr Lys Ala Ile Thr Cys Glu Ala Asn Met Pro Thr Leu Val Asp Gln		
275	280	285
Gly Phe Trp Ile Gly Gly Gln Tyr Ala Leu Thr Pro Thr Ser Leu Pro		
290	295	300
Gln Tyr Asp Val Ser Glu Ala Tyr Ala Leu His Thr Leu Thr Phe Ala		
305	310	315
Arg Pro Ser Ser Ala Ala Ala Leu Ala Phe Val Trp Ala Gly Leu Pro		
325	330	335
Gln Gly Gly Thr Ala Pro Ala Gly Thr Pro Ala Trp Glu Gln Ala Ser		
340	345	350
Ser Gly Gly Tyr Leu Thr Trp Arg His Asn Gly Thr Thr Phe Pro Ala		
355	360	365
Gly Ser Val Ser Tyr Val Leu Pro Glu Gly Phe Ala Leu Glu Arg Tyr		
370	375	380
Asp Pro Asn Asp Gly Ser Trp Thr Asp Phe Ala Ser Ala Gly Asp Thr		
385	390	395
Val Thr Phe Arg Gln Val Ala Val Asp Glu Val Val Val Thr Asn Asn		
405	410	415
Pro Ala Gly Gly Ser Ala Pro Thr Phe Thr Val Arg Val Pro Pro		
420	425	430
Ser Asn Ala Tyr Thr Asn Thr Val Phe Arg Asn Thr Leu Leu Glu Thr		
435	440	445
Arg Pro Ser Ser Arg Arg Leu Glu Leu Pro Met Pro Pro Ala Asp Phe		
450	455	460
Gly Gln Thr Val Ala Asn Asn Pro Lys Ile Glu Gln Ser Leu Leu Lys		
465	470	475
Glu Thr Leu Gly Cys Tyr Leu Val His Ser Lys Met Arg Asn Pro Val		
485	490	495
Phe Gln Leu Thr Pro Ala Ser Ser Phe Gly Ala Val Ser Phe Asn Asn		
500	505	510
Pro Gly Tyr Glu Arg Thr Arg Asp Leu Pro Asp Tyr Thr Gly Ile Arg		
515	520	525
Asp Ser Phe Asp Gln Asn Met Ser Thr Ala Val Ala His Phe Arg Ser		
530	535	540
Leu Ser His Ser Cys Ser Ile Val Thr Lys Thr Tyr Gln Gly Trp Glu		
545	550	555
Gly Val Thr Asn Val Asn Thr Pro Phe Gly Gln Phe Ala His Ala Gly		
565	570	575
Leu Leu Lys Asn Glu Glu Ile Leu Cys Leu Ala Asp Asp Leu Ala Thr		
580	585	590
Arg Leu Thr Gly Val Tyr Pro Ala Thr Asp Asn Phe Ala Ala Ala Val		
595	600	605
Ser Ala Phe Ala Ala Asn Met Leu Ser Ser Val Leu Lys Ser Glu Ala		
610	615	620
Thr Ser Ser Ile Ile Lys Ser Val Gly Glu Thr Ala Val Gly Ala Ala		
625	630	635
		640

Gln Ser Gly Leu Ala Lys Leu Pro Gly Leu Leu Met Ser Val Pro Gly
645 650 655
Lys Ile Ala Ala Arg Val Arg Ala Arg Arg Ala Arg Arg Ala Ala
660 665 670
Arg Ala Asn
675

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGGGATCCAC AGTTCTGCCT CCCCGGACG GTAAATATAG GGGAACCATG GTCTAGAGG 59